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DB=USPT,PGPB,JPAB,EPAB,DWPI; PLUR=YES; OP=OR			
L7	l2 and (pro$).ab.	25	L7
L6	l1 and ($mg.2).ab.	0	L6
L5	pro-c-mg$	0	L5
L4	"pro-c-mg.2"	0	L4
L3	L2 and (polypep$ OR protein).ab.	37	L3
L2	L1 and (angiogen$).ab.	39	L2
L1	(gerritsen-m$ or goddard-a$ or grimaldi-j$ or mehraban-f$).in.	212	L1

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NEWS 17 Apr 22 BIOSIS Gene Names now available in TOXCENTER
NEWS 18 Apr 22 Federal Research in Progress (FEDRIP) now available
NEWS 19 Jun 03 New e-mail delivery for search results now available
NEWS 20 Jun 17 MEDLINE Reload
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  54 FILES SEARCHED...
L1   11 "PRO-C-MG.2"

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L2   10 DUP REM L1 (1 DUPLICATE REMOVED)

=> d l-1

L2   ANSWER 1 OF 10 PROMT COPYRIGHT 2002 Gale Group

ACCESSION NUMBER: 2001:372498 PROMT
TITLE: COMPANY.
SOURCE: Implement & Tractor, (Annual 2001) pp. 4.
                     ISSN: 0019-2953.
PUBLISHER: Freiburg Publishing Co. Inc.
DOCUMENT TYPE: Newsletter
LANGUAGE: English
WORD COUNT: 78063
                     FULL TEXT IS AVAILABLE IN THE ALL FORMAT

L2   ANSWER 2 OF 10 CAPLUS COPYRIGHT 2002 ACS   DUPLICATE 1
AN   2001:265bf4 CAPLUS
DN   134:291146
TI   Human polypeptides and their encoding nucleic acids for use in angiogenesis and vascularization
IN   Gerritsen, Mary E.; Goddard, Audrey; Grimaldi, J. Christopher; Menrabar, Fuad
PA   Genentech, Inc., USA; Curagen Corporation
SO   PCT Int. Appl., 193 pp.
     CODEN: PIXXD2
DT   Patent

LA English
FAM.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2001025433	A2	20010412	WO 2000-US27011	20001004
	AU 2001027437	A5	20010507		

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM

RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

PRAI US 1999-155587P P 19991007
US 1999-162611P P 19991028

L2 ANSWER 3 OF 10 PROMT COPYRIGHT 2002 Gale Group

ACCESSION NUMBER: 2001:152547 PROMT
TITLE: Manufacturers.
SOURCE: Canadian Machinery and Metalworking, (Dec 2000) Vol. 95, No. 10, pp. 103.
ISSN: 0008-4379.
PUBLISHER: Maclean Hunter Canadian Publishing Ltd.
DOCUMENT TYPE: Newsletter
LANGUAGE: English
WORD COUNT: 6478
FULL TEXT IS AVAILABLE IN THE ALL FORMAT

L2 ANSWER 4 OF 10 PROMT COPYRIGHT 2002 Gale Group

ACCESSION NUMBER: 2001:453282 PROMT
TITLE: COMPANY.(Buyers Guide)
SOURCE: Implement & Tractor, (Annual 2000) pp. 4.
ISSN: 0019-2953.
PUBLISHER: Freiburg Publishing Co. Inc.
DOCUMENT TYPE: Newsletter
LANGUAGE: English
WORD COUNT: 81211
FULL TEXT IS AVAILABLE IN THE ALL FORMAT

L2 ANSWER 5 OF 10 DGENE (C) 2002 THOMSON DERWENT
AN AAE02775 Protein DGENE
TI Polypeptides critical for angiogenesis and vascularization, and the nucleic acids encoding them, useful for treating conditions related to inappropriate vascularization and angiogenesis -
IN Gerritsen M E; Goddard A; Grimaldi J C; Mehraban F
PA (GETH) GENENTECH INC.
(CURA-N) CURAGEN CORP.
PI WO 2001025433 A2 20010412 [illegible]
AI WO 2000-US27011 20001004
PRAI US 1999-155587P 19991007
US 1999-162611 19991028
DT Patent
LA English
OS 2001-167229 [34]

L2 ANSWER 6 OF 10 DGENE (C) 2002 THOMSON DERWENT

AN [illegible] DNA DGENE
TI Polypeptides critical for angiogenesis and vascularization, and the nucleic acids encoding them, useful for treating conditions related to inappropriate vascularization and angiogenesis -
IN Garrison M E; Goddard A; Grimaldi J C; Mehraban F
PA (GETH) GENENTECH INC.
(CURA-N) CURAGEN CORP.
PI WO 200102551[illegible] A2 20010412 169p
AI WO 2000-US27512 20001005
PRAI US 1999-158587 19991007
US 1999-162611 19991028
DT Patent
LA English
CS [illegible]-36722 [38]

L2 ANSWER 7 OF 10 DGENE (C) 2002 THOMSON DERWENT
AN AAD07047 DNA DGENE
TI Polypeptides critical for angiogenesis and vascularization, and the nucleic acids encoding them, useful for treating conditions related to inappropriate vascularization and angiogenesis -
IN Garrison M E; Goddard A; Grimaldi J C; Mehraban F
PA (GETH) GENENTECH INC.
(CURA-N) CURAGEN CORP.
PI WO 200102551[illegible] A2 20010412 189p
AI WO 2000-US27512 20001005
PRAI US 1999-158587 19991007
US 1999-162611 19991028
DT Patent
LA English
CS [illegible]-36722 [38]

L2 ANSWER 8 OF 10 DGENE (C) 2002 THOMSON DERWENT
AN AAD07046 DNA DGENE
TI Polypeptides critical for angiogenesis and vascularization, and the nucleic acids encoding them, useful for treating conditions related to inappropriate vascularization and angiogenesis -
IN Garrison M E; Goddard A; Grimaldi J C; Mehraban F
PA (GETH) GENENTECH INC.
(CURA-N) CURAGEN CORP.
PI WO 200102551[illegible] A2 20010412 189p
AI WO 2000-US27512 20001005
PRAI US 1999-158587 19991007
US 1999-162611 19991028
DT Patent
LA English
CS [illegible]-36722 [38]

L2 ANSWER 9 OF 10 DGENE (C) 2002 THOMSON DERWENT
AN AAD07045 DNA DGENE
TI Polypeptides critical for angiogenesis and vascularization, and the nucleic acids encoding them, useful for treating conditions related to inappropriate vascularization and angiogenesis -
IN Garrison M E; Goddard A; Grimaldi J C; Mehraban F
PA (GETH) GENENTECH INC.
(CURA-N) CURAGEN CORP.
PI WO 200102551[illegible] A2 20010412 189p
AI WO 2000-US27512 20001005
PRAI US 1999-158587 19991007
US 1999-162611 19991028
DT Patent

LA English
OS 2001-367229 [38]

L2 ANSWER 1 OF 10 DGENE (C) 2002 THOMSON DERWENT
AN AAD07643 cDNA DGENE
TI Polypeptides critical for angiogenesis and vascularization, and the nucleic acids encoding them, useful for treating conditions related to inappropriate vascularization and angiogenesis -
IN Gerritsen M E; Goddard A; Grimaldi J C; Menrahan F
PA (GETH) GENENTECH INC.
(CURA-N) CURAGEN CORP.
PI WO 20010754333 A2 20010412 lspp
AI WO 2000-US27512 20001005
PRAI US 1999-158587 19991007
US 1999-162611 19991028
DT Patent
LA English
OS 2001-367229 [38]

GenCore version 4.5

M protein - protein search, using sw model

Run on: [illegible] ; Search time 66.81 Seconds
(without alignments)
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Title: US-09-684-458-2
Perfect score: [illegible]
Sequence: [illegible]

Scoring table: BLOSUM62
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SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
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2	[illegible]	4.5	[illegible]	1	KIK1_YEAST	q12236 saccharomyce
3	[illegible]	4.5	968	1	STK1_MOUSE	o55098 mus musculu
4	[illegible]	5.7	1895	1	YLK3_CAEEL	P41951 caenorhabdi
5	[illegible]	5.6	736	1	KPCE_RABIT	P10830 oryctolagus
6	[illegible]	5.6	737	1	KPCE_HUMAN	q02156 homo sapien
7	[illegible]	5.5	737	1	KPCE_MOUSE	P16054 mus musculu
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9	[illegible]	5.3	411	1	SNX1_RAT	P57269 rattus norv
10	[illegible]	5.3	771	1	PKEA_PHYBL	q31377 phycomyces
11	[illegible]	5.2	741	1	Y587_HUMAN	Q92585 homo sapien
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15	[illegible]	5.1	1247	1	SOS2_MOUSE	Q62384 mus musculu
16	[illegible]	5.1	1258	1	SNX6_HUMAN	Q9Y5W8 homo sapien
17	[illegible]	5.0	1101	1	EGA2_HUMAN	P60879 homo sapien
18	[illegible]	4.9	1252	1	ERB2_RAT	P06494 rattus norv
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20	[illegible]	4.8	672	1	KPC9_HUMAN	Q05655 homo sapien
21	[illegible]	4.8	1255	1	ERB2_HUMAN	P04626 homo sapien
22	[illegible]	4.8	1791	1	YAV_SCHPO	Q10172 schizosacch
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24	[illegible]	4.7	113	1	STK6_HUMAN	Q9Y6E0 homo sapien
25	[illegible]	4.7	[illegible]	1	SPKD_SYNY3	P54785 synechocyst
26	[illegible]	4.7	682	1	SPL1_CAEEL	P46549 caenorhabdi
27	[illegible]	4.6	748	1	KPC2_APLCA	Q16975 aplysia cal
28	[illegible]	4.6	426	1	STK5_HUMAN	Q00506 homo sapien
29	[illegible]	4.6	774	1	KPC2_MOUSE	P28867 mus musculu
30	[illegible]	4.6	745	1	AFC_MEVAR	P30521 abelson mur
31	[illegible]	4.5	978	1	BNR1_YEAST	P43450 saccharomyce
32	[illegible]	4.5	842	1	CLA1_YEAST	P36062 saccharomyce
33	[illegible]	4.5	1332	1	SOS2_HUMAN	Q07889 homo sapien
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36	137	4.6	939	1	STE7_YEAST	P38497 saccharomyce
37	137	4.6	1254	1	ERB2_MESAU	P70538 mesocricetu
38	137	4.6	1273	1	MYS3_YEAST	P36006 saccharomyce
39	137	4.6	1567	1	PMN2_MOUSE	Q91104 mus musculu
40	136	4.5	869	1	CD5S_MOUSE	O35926 mus musculu
41	136	4.5	426	1	STK5_MOUSE	Q9Z2W1 mus musculu
42	136	4.5	501	1	WASL_RAT	Q88836 rattus norv
43	135.5	4.5	585	1	WASL_BOVIN	Q95137 bos taurus
44	135.5	4.5	634	1	KPC3_DROME	P34928 drosophila
45	134.5	4.5	474	1	SNXE_HUMAN	Q9Y5W7 homo sapien

ALIGNMENTS

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RESULT   1
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ID   STK1_HUMAN      STANDARD;       PRT:   968 AA.
AC   O94804; Q9UIW4;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Serine/threonine-protein kinase 1  (EC 2.7.1.-) (Lymphocyte-oriented
DE   kinase).
GN   STK10 OR LOK.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99216434; PubMed=10099412;
RA   Furumoto S., Matsuda Y., Okamoto M., Kitamura K., Yokokawa H.,
RA   Karasuyama H.;
RT   "Molecular cloning of the human gene STK1 encoding lymphocyte-
RT   oriented kinase, and comparative chromosomal mapping of the human,
RT   mouse, and rat homologues.";
RL   Immunogenetics 49:369-375(1999).
RN   [2]
RP   SEQUENCE OF 814-968 FROM N.A.
RC   TISSUE=Testis;
RA   Bloecker H., Boecher M., Brandt P., Mewes H. W., Gassenhuber J.,
RA   Wiemann S.;
RL   Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: CAN ACT ON SUBSTRATES BOTH AT SER/THR AND TYR (DUAL
CC       SPECIFICITY) KINASE) AND EXHIBITS AUTOPHOSPHORYLATION (BY SIMILARITY).
CC   -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC   -!- TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN LYMPHOCYTES.
CC   -!- PTM: AUTOPHOSPHORYLATED (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE STE20 FAMILY OF PROTEIN KINASES.
CC       STE20 SUBFAMILY.
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CC   -----------------------------------------------------------------------
DR   EMBL; AB015718; BAA35073.1; -.
DR   EMBL; AL133081; CAB61406.1; -.
DR   HSSP; P24941; 1BCL.
DR   MIM; 603919; -.
DR   InterPro; IPR000719; Euk_pkinase
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR001245; Tyr_pkinase
DR   Pfam; PF00069; pkinase; 1.
DR   PRINTS; PR00109; TYRKINASE.
DR   SMART; SM00220; S_TKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
```

```
ID   [illegible] STANDARD; PRT; [illegible] AA.
DT   [illegible], REL. 11, CREATED)
DT   [illegible], REL. 11, DATA UPDATED)
DE   [illegible] protein kinase; ATP binding;
KW   [illegible] coiled coil.
FT   DOMAIN       [illegible]     PROTEIN KINASE.
FT   DOMAIN       573     647     COILED COIL (POTENTIAL).
FT   DOMAIN       [illegible]     GLN RICH.
FT   NP_BIND      45      50      ATP (BY SIMILARITY).
FT   BINDING      65      65      ATP (BY SIMILARITY).
FT   ACT_SITE     157     157     BY SIMILARITY.
SQ   SEQUENCE   968 AA;  111234 MW;  15E24513BE0C553D CRC64;


  Query Match          6.6%;  Score 199.5;  DB 1;  Length 968;
  Best Local Similarity   24.2%;  Pred. No. 0.00043;
  Matches  123;  Conservative   60;  Mismatches  184;  Indels  141;  Gaps   25;

Qy      113 EQVRKITKQNNYGANYIIAIQQLVCMFTYCILFKWLVVLFLKDIGWKIPEEAFLIMKKLKNQF 172
            .  .. ...                              ||:|  | |       |  | ||
Db       34 EHVERCGLDENEV                          WEIVGKLGDG  GAFGKVY  KAKN-- 55

Qy      173 KEPLVLQWAIEGPDKYLGG KDFQQCLIKLLPSCIHPYIYRVIFATANESSALLIRMFNEK 231
            ::  :  : :  |   : :|:   |:|| || ||| ::  |  :   ::  |
Db       56 KETIAIAAAKVIETKSTAEEIEDFYIVETKILAPCIHPYIVKLIGAYYHDGKLWIMIEFCPG 115

Qy      232 TLRQVADHRYRAPGIAIQTPPVSNGFFQQPTQLLLDLIHRDPTLVYGHLHA 281
            :  :  :                  :||   ||:   ||:|| | |:|  :  : | |
Db      116 SAVDAIMLELG                 KGLTEPQIQVVCRQMLEALNFLHSKRIIHRDLKAG 160

Qy      282 [illegible]                 PCPLLDLENSLLVQLSDYGYPEPPEKINSLL      C 332
            :  :  :                    : |   :| :| | :     :     |::
Db      161 [illegible]                 KGLLDLEVICKLADFGLARQMDPCNLSVLHSLPVFENLTA 217

Qy      333 VCVHCPCHLIYEMIYGRPP  DGVPV        DSPPP   APSMAVVAVCLSILSCFAC 380
            |:  :  :  :|   ||  :  |:          | ||    ||   |     |
Db      218 ATWCKLLLVDPKAQIPPPPPPETNIMMVVELMAACTHRLLELDPSERWCVL EEALLKIALE 277

Qy      381 KN  SMPLSPFL_MPLEGDVLLTTSEKPQKKIPLKLAAMKIAKRHTWEKPLIEPQKQTH 438
            .. .  :  :  :  :  :  ||  |           |||   :  :  :  |  :::
Db      278 KNLIPPGAA_LLEHPFVSSI   ISNK           AIR   ELVAEAKAFVMEEIE 319

Qy      439 GDKEILEA_GHPCCEEEPKKPKLLARKKSKRPCALSNCDDDCARYCNCNNGGVCASDPL P 497
            |       :  :|:                  | |||  :|:|  |  :     |  ||
Db      320 [illegible]       DESEEEL          AVDAASILENHIQNSSEVSPPS-  INADKPLEE 360

Qy      498 CL_CCCCCC               LSGISALPPPPPPPPPEP       AAPLP      PASTEV 544
                                   :|  :|    ||  :     | |:|      | | :
Db      361 [illegible]AES_S_LSVNEPSSQPSSGDKSLQLESPPVVAPCNENGLAVPVPLKKSRPVSMDA 420

Qy      545 PA_LSSQAVNGMSPGALESSTQNPQKGL 572
            :  :  :  :  :  :  :  :  || :
Db      421 PL_VA_EK_VAP_GRGSPAANRSQKAS 448


RESULT 2
P48360
ID   KPKO_YEAST      STANDARD;      PRT;   [illegible] AA.
AC   P48360;
DT   01-NOV-1996 (Rel. 35, Created)
DT   01-NOV-1996 (Rel. 35, Last sequence update)
DT   [illegible] (Rel. 11, Last annotation update)
DE   Serine/threonine protein kinase YOL100W (EC 2.7.1.-).
GN   YOL100W OR BF6.01.
OS   Saccharomyces cerevisiae (Baker's yeast).
OC   Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
OC   Saccharomycetaceae; Saccharomyces.
OX   NCBI_TaxID=4932;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96176641; PubMed=7502582;
RA   Vandenbol M., Jauniaux J.C., Portetelle D., Hilger F.;
RT   "Sequence analysis of a 44 kb DNA fragment of yeast chromosome XV
RT   reveals the lys1 H3 retrotransposon, the sut1(+) frameshift
RT   suppressor gene for tRNA Gly, the yeast transfer RNA thr-1a and a
RT   delta element.";
RL   Yeast 11:1069-1075(1995).
CC   -!- SIMILARITY: BELONGS TO THE SER/THR PROTEIN KINASE FAMILY.
CC       PKC SUBFAMILY.
CC   ---------- -- --------- - - ------- ---- - - -
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CC   ---------- -- --------- - - ------- ---- - - -
DR   EMBL; Z48149; CAA88162.1; -.
DR   EMBL; Z74842; CAA99113.1; -.
DR   HSSP; P00517; 1SPC.
DR   SGD; S0005460; YOL100W.
DR   InterPro; IPR000719; Euk_pkinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   Pfam; PF00069; pkinase; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW   Hypothetical protein; Transferase; Serine/threonine protein kinase;
KW   ATP binding.
FT   DOMAIN      179     443       PROTEIN KINASE.
FT   NP_BIND     185     193       ATP (BY SIMILARITY).
FT   BINDING     208     208       ATP (BY SIMILARITY).
FT   ACT_SITE    303     303       BY SIMILARITY.
SQ   SEQUENCE   [illegible] AA;  [illegible] Mw;  [illegible] CRC64;


  Query Match          6.5%;  Score 195;  DB 1;  Length 1081;
  Best Local Similarity   21.4%;  Pred. No. 0.00087;
  Matches  103;  Conservative   74;  Mismatches  161;  Indels  144;  Gaps   20;

Qy      191 EEYELMKKLGQGTFGEVFLVEWAKDRKTGEKVALKRVRLQDFEPESVRFMAREILILRRLNHQ 250
            ||:  :  |:|  ||  ||          ||||:  :  '||  |   |  :|:|     :|
Db      202 EEMYAAEVLN  ++EYLIM---  EEVFSVGHLR  AEQEILNNS  +  DSVVRLFSTFQDES 261

Qy      251 SALGIEMLEGNLLKLRSRLRTEAFCPEIPEDGETMEFLQSIVSRVSKGLPFVASKIYSYFTDL 310
            |  :  :  |  |:  |  |  |  :|              |  ||:: : :||
Db      262 SLYFLLEYAPNGDFLSLMKKYGSLDETCARY          --  --  -- YAAQITDALDYLH 305

Qy      311 DKGFPYGHLHASNVMLDGH          EPELLLLDNGLLGLPSPYKSYESLPRKCNELP 371
              |  :  :  |::|||:          | :|||:  :: :  :  |  :  : | |
Db      306 SNGIIHRDIKPENILLDKDMRIKLCDFGLACKLNPNNVKYHSYVATRWYRSPELLVGDTE SEVGIAE 374

Qy      372 GV                DVIDCFGCLLYEMCYGKPLFSGVEVD              GGTEAFGN 415
              |                |:  || :|:::|  :|||     :              :| :  :
Db      375 YVSFLLSLRLLSYHLSWASL  :::|_MAFLRSFLRAGNSDPLRVMKVQVYAFIPDPDL 434

Qy      416 AVVAVLESILSCEACKN--GMPLISRLLQMPLPSIVLL  -      PISERKLPKPIPK 473
            :  :::  |    ||     ||||:  :  | |:            |  |   :|:  |
Db      435 LIKDGVRKIL    VRGLLSRSP--QNRPSMREVLEMSWLNEKGCVWDRPIFICPEYFENAPES 492

Qy      474 KEALE------RIAKEGI----EKRLIEEQK      -  QTHQHRRPLTPAQSHRCSEPERKKR 529
            :|:      :: |: :     :  |: ::      :  :  |   :|  :|  :| :  :
Db      493 MQAMPGSTPKEVFKSVNLLDKGPTPVLGSGAQGSVFLVEMIDNQTLYRMKHAATEGGSLK 552

Qy      530 KILARKKSSRKSAC-LEN--                          SEEHSARYSNSSN 580
            |   |   :|:|  |||                           :::     |  |:
Db      553 K   EPTPEEIAQILENAERGLNNERNGIPGFKSEIKFAALAAGLAALEKEIMQSYFISS 607

Qy      581 NSGSGASSPLIS---------      -PSSPIPE SISGISALPPPPPPPPPPAAFLPPA 630
            :  | :||: |:                 | : :|:  :  |  :|:  |  |:  :| : |:|
Db      608 SKSSKSSSPAFISKPGIYKKISSISSKRPAASFLSASVLSSKVIMFFGIFMSLEMIFT 667

Qy      631 ST 632
            |
Db      668 DT 669
```

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RESULT     3
ST10_MOUSE
ID   ST10_MOUSE     STANDARD;      PRT;   966 AA.
AC   O55098;
DT   [illegible]-2001 (Rel. 40, Created)
DT   [illegible]-2001 (Rel. 40, Last sequence update)
DT   [illegible]-2001 (Rel. 40, Last annotation update)
DE   Serine/threonine protein kinase 10 (EC 2.7.1.37) (Lymphocyte-oriented
DE   kinase).
GN   STK10 OR LOK.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID [illegible];
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Thymus;
RX   MEDLINE=97420413; PubMed=9278426;
RA   Kuramochi S., Moriguchi T., Kuida K., Endo J., Semba K., Nishida E.,
RA   Karasuyama H.;
RT   "LOK is a novel mouse STE20-like protein kinase that is expressed
RT   predominantly in lymphocytes.";
RL   J. Biol. Chem. 272:22679-22684(1997).
CC   -!- FUNCTION: CAN ACT ON SUBSTRATES SUCH AS MYELIN BASIC PROTEIN AND
CC       HISTONE H1A ON SERINE AND THREONINE RESIDUES.
CC   -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC   -!- TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN LYMPHOID ORGANS
CC       SUCH AS SPLEEN, THYMUS, AND BONE MARROW.
CC   -!- PTM: AUTOPHOSPHORYLATED.
CC   -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC       STE20 SUBFAMILY.
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CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; [illegible]; BAA[illegible].1; -.
DR   HSSP; [illegible]; [illegible].
DR   MGD; MGI:[illegible]; Stk10.
DR   InterPro; IPR000719; Euk_pkinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   Pfam; PF00069; pkinase; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW   Transferase; Serine/threonine-protein kinase; ATP-binding;
KW   Phosphorylation; Coiled coil.
FT   DOMAIN       [illegible]    2[illegible]       PROTEIN KINASE.
FT   DOMAIN       [illegible]    [illegible]       COILED COIL (POTENTIAL).
FT   DOMAIN       749    853       GLN-RICH.
FT   NP_BIND       42     50       ATP (BY SIMILARITY).
FT   BINDING       65     65       ATP (BY SIMILARITY).
FT   ACT_SITE     157    157       BY SIMILARITY.
SQ   SEQUENCE   966 AA;  111[illegible] MW;  7115EAC0103[illegible]28F94 CRC64;

  Query Match             [illegible]%;  Score 80.5;  DB 1;  Length 966;
  Best Local Similarity   24.8%;  Pred. No. 0.004[illegible];
  Matches  [illegible];  Conservative   [illegible];  Mismatches  172;  Indels  125;  Gaps   22;

Qy        11[illegible] EIVKK[illegible] [illegible] 172
Db         [illegible] EEVRPE[illegible]PNEA          WEIVGELGD  GAPGKVY  KAKN   55

Qy        17[illegible] KEEVLVESWALG[illegible]KYLSD[illegible]KDEQ[illegible]LIKILPS[illegible]HPYIYRV[illegible]FATANSSALLIRMENEK 231

Db         56 KETGALAAAKVIETKSEEELEDYIVEIEILATCDHPYIVKLLGAYYYDGKLWIMIEFCPG 115

Qy        232 CTLKDLIYKAKP[illegible]LKKYCNPKK[illegible] 291
Db        116 GAVDAIMLELD[illegible]RGLNEPQIQVVCRQMLEALNFLHCKRIIHRDLKA 160

Qy        292 SNVM  LLGD[illegible]RLLDLENSLLGR[illegible]SQFPKINILEGV [illegible] 334
Db        161 GNVLMTLEGDIRLADFGVSAKNLKTL[illegible]WMAPEVVMCETMKDAPYDYKAD 219

Qy        335 VHCFGHLLYIMTTGKPF  D[illegible]V[illegible]V [illegible] 383
Db        220 IWSLGITLIEMAQIEPPHHELNPMRVLLKIAKSDPPTLLTPSKWSVEFRDFLKIALDKN 278

Qy        384 --CMPTISRLLQMPLPSDVLLIISEKL[illegible] 440
Db        279 PETRPSAAQLLQHPFVSRV---TSNK-----   ---ALR   ELVAEAKAEVMEEIEDG 321

Qy        441 EELIEAQ[illegible]HIE[illegible]LLEEKKEKILAEEKL[illegible]SPS 500
Db        322 R-------EDGEEEDAV-------  -     LAVEPLVNSHLQ[illegible]ANVIQL[illegible]DSNKLLQSS 362

Qy        501 SPTFPSTSG[illegible]SALFPPPPPPPPPAAPL[illegible]LAVNGMSR 548
Db        363 TPLPPS-          ----QPQEPVNGP[illegible]SQPSG[illegible]GELQTISLA [illegible]GLSK 398


RESULT      4
YLK3_CAEEL
ID   YLK3_CAEEL     STANDARD;      PRT;   1[illegible] AA.
AC   P41951;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   Putative serine/threonine-protein kinase D1044.3 in chromosome III
DE   (EC 2.7.1.-).
GN   D1044.3.
OS   Caenorhabditis elegans.
OC   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC   Rhabditidae; Peloderinae; Caenorhabditis.
OX   NCBI_TaxID=6239;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BRISTOL N2;
RA   Pauley A., Waterston R.;
RL   Submitted (JUN-1994) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC       STRONG, TO ZC84.1.
CC   --------------------------------------------------------------------------
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CC   --------------------------------------------------------------------------
DR   EMBL; U00065; AAA50735.1; -.
DR   HSSP; Q63450; 1A06.
DR   WormPep; D1044.3; CE01206.
DR   InterPro; IPR002899; EB.
DR   InterPro; IPR000719; Euk_pkinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   Pfam; PF01683; EB; 12.
DR   Pfam; PF00069; pkinase; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   SMART; SM00289; WR1; 12.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW   Hypothetical protein; Transferase; Serine/threonine-protein kinase;
KW   ATP-binding.
FT   DOMAIN      431    703       PROTEIN KINASE.
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FT   NP_BIND      414    421       ATP (BY SIMILARITY).
FT   BINDING      436    436       ATP (BY SIMILARITY).
FT   ACT_SITE     531    531       BY SIMILARITY.
SQ   SEQUENCE   736 AA;  83515 MW;  2610C4FEE59E9BFEB CRC64;


  Query Match          5.2%;  Score 170.5;  DB 1;  Length 1895;
  Best Local Similarity   21.8%;  Pred. No. 0.041;
  Matches  134;  Conservative   96;  Mismatches  289;  Indels  225;  Gaps   40;

Qy      44 IRVLRGV        SVENG        WQIVRKYSSDFDLLENNSLQIACLSL        PLP  76
                :  :        : : :        :  :  :     :     :: : :        : :
Db     259 IPIYIGVPEELKDELSTENCPKLQWHVAWFLAGLAMCHELSLEIAQLSGSLIFAAISNPKP  285

Qy      77 IKKCLTNMSFSGIA                  EPQKDLQN     YI          NVIIDNR  107
                :  :  :                    :  : :       :          : : :
Db     286 IQEAVI     LWVAMLSSLIALLAGLAGACNQGLMCNANGVYIIGKLIAIKKNVIIDET  341

Qy     108 LSN                            ELVKKPLLSPNNYSA   NYIEIAIQQ  145
               : :                          : :::: ::::   :: :::
Db     342 IGWLIQVSIFFVLKLMYIFDKSRQLLKKVLSIGIFPVIVNYNRNVLIIYSQIAKHY  401

Qy     146 VSMG    EGSIFKWEVV                EPEKDPG        WEIKEEVIDKLKNQF  192
                   :                         : : :         : :::              :
Db     402 LNCTEENIEIMKLWEIVNEFLGAVDVGKEDDDQVSAGAEGVYIVRKK   AGSHSLNP  459

Qy     193 KEPVLI    WGLSSIEKVLSLIEEQTLI    PIIIPI  EPYI   YPVTIAIANLPAL  237
                 :    :   : :::: : :  :::    : :: :  :  :   : :  :    :  :
Db     460 APILALKEFIMINLNRPE   SGKSPCDMISEVKIIKQLLRHPNIVKYREIFV    ENHKL  514

Qy     238 TRMENEKKIIKLIYKAKPPEIPKEKV NPKKIIALENLQYCEIFVLKPLH  281
               : :::::   : :    :     :::  : :       :::  :::::
Db     515 YIVMEYASGGEVFDYLVAHGRMKEKEARAKFRQIVSAVQYCHQKFIVHRDL  564

Qy     282 KIPEYRHISAGNVMLSEDDTPELLDFNISIAIG      PSFYRS      YFSQPFKKINIL  330
               :  :  :  :  :  :  :  :  :  :  :      :  :      :  :  :  :  :
Db     565 KLIVDEDDKLKIIDFGLAAKLKPDERQSKAAVGTPAYMSPEVVLGKEYDAKVDIWSIGVIL  624

Qy     331 GLIDHDNRLKLHIMSVQDVDSFPVDSPFYRSLIEESVRACKNGMFTS  378
              :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db     625 YICLSGYPPFSEHRTQVSLKDQITSGKYNFIPEVWAEVSEKALDLVKK  672

Qy     379 LTYFGLVRLKAEEAVTGAESLTHTLDRGLKFTIRDQLVKGSMDGLVS  426
              :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db     673 LLVVDPKARFTTEEALRHPWLQDEDMKRKFQDLLSEENESTTAVESV  720

Qy     427 EIMDMGNIASDIEIMLAQQVTEVMLSLTSMEFDYIVDCVAIGNGFVE  474
              :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db     721 DSSNSNSLMTPFSFVTPDFLQEIQGSVACCHYHPVTAEINIDDGDSE  768

Qy     475 DRITGSLCKLAHLFHHVYNGEVPTPLMPQTLRE     RKETEERG          PEYAAEVIEALM  520
              :  :  :  :  :  :  :  :  :  :  :      :  :  :          :  :  :  :
Db     769 DTTLHSMEKASQLSMQSSSARTPSQDAAIEIRS     KSSAVDLTGYGEAITMTGETVDLDLY  818

Qy     521 SKGELFGYAGLGPPSWKPALGGLGIELKGVEKPVAGHKVDLKLYTMDAFEGWQAIDQVIQF  580
              :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db     819 SKGELFGYAGLGPPSWKPALGGLGIELKGVEKPVAGHKVDLKLYTMDAFEGWQAIDQVIQF  878

Qy     581 LEEPMMNVSSPWFKPLEGSPAEREDAPLVRTLSQMHLARGFSLEAKSGSTSNDMVLTNPTP  640
              :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db     879 LEEPMMNVSSPWFKPLEGSPAEREDAPLVRTLSQMHLARGFSLEAKSGSTSNDMVLTNPTP  938

Qy     641 QSKSVSTPIMIAEGAESATDSTLMQVGYLAHNIKNEVDPQEERMRSEEAIRVTSDLIQNYL  700
              :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db     939 QSKSVSTPIMIAEGAESATDSTLMQVGYLAHNIKNEVDPQEERMRSEEAIRVTSDLIQNYL  998

Qy     701 LKARMIAIELDKVIEFMQYNQKIQVREKMGSMVHDFKVMNTELEGFLAEKRQDQEFLKSMF  760
              :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db     999 LKARMIAIELDKVIEFMQYNQKIQVREKMGSMVHDFKVMNTELEGFLAEKRQDQEFLKSMF 1058

Qy     761 LFDKNRDGFIDRNELEDMLVALNMRDGDKGLTPIQVEEIIDNVLLTTNQIDFDGFLTMMVS  820
              :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db    1059 LFDKNRDGFIDRNELEDMLVALNMRDGDKGLTPIQVEEIIDNVLLTTNQIDFDGFLTMMVS 1118

Qy     821 KEMPATEAEQIAAAFKMFDKDGNGYISAAELRHVMTNLGEKLTDEEVDEMIREADIDGDGQ  880
              :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db    1119 KEMPATEAEQIAAAFKMFDKDGNGYISAAELRHVMTNLGEKLTDEEVDEMIREADIDGDGQ 1178

Qy     881 VNYEEFVQMMTAK  893
              :  :  :  :  :
Db    1179 VNYEEFVQMMTAK 1191


RESULT   5
P07814 PARG1
ID   RPC1_PARLI     STANDARD;      PRT:   736 AA.
AC   P07814;
DT   01-OCT-1988 (Rel. 07, Created)
DT   01-OCT-1988 (Rel. 07, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Protein kinase C, epsilon type (EC 2.7.1.-) (PKCE) (Fragment).
OS   PARLI
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX   NCBI_TaxID=9986;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE 88223367; PubMed 3370672;
RA   Ohno S., Akita Y., Konno Y., Imajoh S., Suzuki K.;
RT   "A novel phorbol ester receptor/protein kinase, nPKC, distantly
RT   related to the protein kinase C family.";
RL   Cell 53:731-741(1988).
CC   -!- FUNCTION: THIS IS CALCIUM INDEPENDENT, PHOSPHOLIPID DEPENDENT,
CC       SERINE- AND THREONINE-SPECIFIC ENZYME.
CC   -!- FUNCTION: PKC IS ACTIVATED BY DIACYLGLYCEROL WHICH IN TURN
CC       PHOSPHORYLATES A RANGE OF CELLULAR PROTEINS. PKC ALSO SERVES AS
CC       THE RECEPTOR FOR PHORBOL ESTERS, A CLASS OF TUMOR PROMOTERS.
CC   -!- SIMILARITY: CONTAINS 2 ZINC DEPENDENT PHORBOL ESTER AND DAG
CC       BINDING DOMAINS.
CC   -!- SIMILARITY: CONTAINS 1 C2 DOMAIN.
CC   -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC       PKC SUBFAMILY.
CC   ---------- ------- --- ---- ---- ---- ---
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CC   entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------- ------- --- ---- ---- ---- ---
DR   EMBL; M20014; AAA31426.1; -.
DR   PIR; A29868; KIRBCE.
DR   HSSP; P28867; 1PFQ.
DR   InterPro; IPR000008; C2.
DR   InterPro; IPR002219; DAG_PE-bind.
DR   InterPro; IPR000719; Prot_pkinase.
DR   InterPro; IPR000961; Pkinase_C.
DR   InterPro; IPR002290; ser_thr_pkinase.
DR   Pfam; PF00168; C2; 1.
DR   Pfam; PF00130; DAG_PE-bind; 2.
DR   Pfam; PF00069; pkinase; 1.
DR   Pfam; PF00433; pkinase_C; 1.
DR   PRINTS; PR00008; DAGPEDOMAIN.
DR   SMART; SM00109; C1; 2.
DR   SMART; SM00239; C2; 1.
DR   SMART; SM00133; S_TK_X; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   PROSITE; PS50004; C2_DOMAIN_2; 1.
DR   PROSITE; PS00479; DAG_PE_BIND_DOM_1; 1.
DR   PROSITE; PS50081; DAG_PE_BIND_DOM_2; 2.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW   Repeat; ATP binding; Transferase; Phosphorylation;
KW   Serine/threonine protein kinase; Phorbol ester binding; Zinc.
FT   DOMAIN        1     99       C2 DOMAIN.
FT   DOMAIN      170    220       PHORBOL ESTER AND DAG BINDING 1.
FT   DOMAIN      243    292       PHORBOL ESTER AND DAG BINDING 2.
FT   DOMAIN      407    667       PROTEIN KINASE.
FT   NP_BIND     414    421       ATP (BY SIMILARITY).
FT   BINDING     436    436       ATP (BY SIMILARITY).
FT   ACT_SITE    531    531       BY SIMILARITY.
FT   MOD_RES     702    702       PHOSPHORYLATION (AUTO ) (POTENTIAL).
FT   MOD_RES     709    709       PHOSPHORYLATION (AUTO ) (POTENTIAL).
SQ   SEQUENCE   736 AA;  83515 MW;  2610C4FEE59E9BFEB CRC64;


  Query Match          5.6%;  Score 168.5;  DB 2;  Length 736;
  Best Local Similarity   23.2%;  Pred. No. 0.017;
  Matches   76;  Conservative   48;  Mismatches  125;  Indels   29;  Gaps   15;

Qy     212 TKPVLIWGLSSIEKVLSLIEEQTLIPIIIPIEPYIYPVTIAIANLPALTRMENEKKIIKL  271
              :  :  :::  :  :   :  :   :  :  :  :  :  :  :  :  :  :  :  :
Db     420 KVMEALKEFIMINLNRPEYLQCLRHEPNIVKYREIFVENHKLYIVMEYASGGEVFDYLVAH  479

Qy     272 IYKAKPPEIPKEKVNPKKIIALENLQYCEIFVLKPLHKIPEYRHISAGNVMLSEDDTPELL  331
              :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db     480 GRMKEKEARAKFRQIVSAVQYCHQKFIVHRDLKAENLLLDADMNIKIADFGFSNEFTFGNK  539

Qy     332 DFNISIAIGPSFYRSYFSQPFKKINILGLIDHDNRLKLHIMSVQDVDSFPVDSPFYRSLIE  391
              :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db     540 LQTFCGSPLYASPEIVNGTPYQGPEVDCWSLGVLMYTLVYGTMPFDGSNFKRLVKQISSG  599

Qy     392 ESVRACKNGMFTSLTYFGLVRLKAEEAVTGAESLTHTLDRGLKFTIRDQLVKGSMDGLVSE  451
              :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db     600 DYREIPDQLSPEAQDLIRRMLTVDPSKRISMKEIRNHPWMQGDLPEYPVNLSDVNLRSCFE  659

Qy     452 IMDMGNIASDIEIMLAQQVTEVMLSLTSMEFDYIVDCVAIGNGFVEDRITGSLCKLAHLFH  511
              :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db     660 DEEPTVLPIQTGKGREIQEIFRDFSLPTPDYEGEVKVLLNDDNQVTLEMATAVKLVCILSH  719

Qy     512 HVYNGEVPTPLMPQTLREGRKETEERGPEYAAEVIEALMSKGELFGYAGLGPPSWKPALGG  571
              :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db     720 PIFEDPVMEYVNGGDLMFQIQRGRLKTDVSFPPHIRQDAELHCLGRMHARVAQMGSTLHSS  779

Qy     572 LGIELKGVEKPVAGHKVDLKLYTMDAFEGWQAIDQVIQFLEEPMMNVSSPWFKPLEGSPAE  631
              :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db     780 LGIELKGVEKPVAGHKVDLKLYTMDAFEGWQAIDQVIQFLEEPMMNVSSPWFKPLEGSPAE  839

Qy     632 REDAPLVRTLSQMHLARGFSLEAKSGSTSNDMVLTNPTPQSKSVSTPIMIAEGAESATDST  691
              :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db     840 REDAPLVRTLSQMHLARGFSLEAKSGSTSNDMVLTNPTPQSKSVSTPIMIAEGAESATDST  899

Qy     692 LMQVGYLAHNIKNEVDPQEERMRSEEAIRVTSDLIQNYLLKARMIAIELDKVIEFMQYNQK  751
              :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db     900 LMQVGYLAHNIKNEVDPQEERMRSEEAIRVTSDLIQNYLLKARMIAIELDKVIEFMQYNQK  959

Qy     752 IQVREKMGSMVHDFKVMNTELEGFLAEKRQDQEFLKSMFLFDKNRDGFIDRNELEDMLVAL  811
              :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db     960 IQVREKMGSMVHDFKVMNTELEGFLAEKRQDQEFLKSMFLFDKNRDGFIDRNELEDMLVAL 1019

Qy     812 NMRDGDKGLTPIQVEEIIDNVLLTTNQIDFDGFLTMMVSKEMPATEAEQIAAAFKMFDKDG  871
              :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db    1020 NMRDGDKGLTPIQVEEIIDNVLLTTNQIDFDGFLTMMVSKEMPATEAEQIAAAFKMFDKDG 1079

Qy     872 NGYISAAELRHVMTNLGEKLTDEEVDEMIREADIDGDGQVNYEEFVQMMTAK  923
              :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db    1080 NGYISAAELRHVMTNLGEKLTDEEVDEMIREADIDGDGQVNYEEFVQMMTAK 1131
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Qy        278 FLHDKGFPYGHLHASNVMLDGD-PCKLLDL                ENSLLGLPSFYRSYFSQF 324
Db        522 FLHQ[illegible]VIYRDLKLDNILLDAE[illegible]CKLADFGMCKEG[illegible]NGVT[illegible]TFCGTPDYIAPEILQ- 57[illegible]

Qy        325 EKINTLESVDVHSFGHLLYEMIYGKPP                 DSVEVDS  [illegible]AFSMAVVAVLE 372
Db        58[illegible]  ELEYG[illegible]VDWWALGVLMYEMMA[illegible]                             [illegible]KLAV[illegible]ILE [illegible]

Qy        37[illegible] S             [illegible]                                VL[illegible]          417
Db        [illegible] AFM[illegible]KN[illegible]                                 WV[illegible]LE[illegible]                VN [illegible]

Qy        418                 --ALKIAKEC[illegible]EKRLIEE[illegible] 434
Db        [illegible] NFDQ[illegible]TREEPVL[illegible]LVDEA[illegible]VKQ[illegible]NQ[illegible] 72[illegible]
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RESULT [illegible]
KPCE_HUMAN
ID   KPCE_HUMAN   STANDARD;   PRT;   737 AA.
AC   Q02156;
DT   [illegible] JUL 1993 (Rel. 26, Created)
DT   [illegible] JUL 1993 (Rel. 26, Last sequence update)
DT   15 JUL 1999 (Rel. 38, Last annotation update)
DE   Protein kinase C, epsilon type (EC 2.7.1.-) (NPKC-epsilon).
GN   PRKCE OR PKCE.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=[illegible];
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=[illegible]; PubMed=1382605;
RA   Basta P., Strickland M.B., Holmes W., Loomis C.R., Ballas L.M.,
RA   Burns D.J.;
RT   "Sequence and expression of human protein kinase C-epsilon.";
RL   Biochim. Biophys. Acta 1132:154-160(1992).
CC   -!- FUNCTION: THIS IS CALCIUM INDEPENDENT, PHOSPHOLIPID DEPENDENT,
CC   SERINE- AND THREONINE-SPECIFIC ENZYME.
CC   -!- [illegible] WHICH IN TURN
CC   PHOSPHORYLATES A RANGE OF CELLULAR PROTEINS. PKC ALSO SERVES AS
CC   THE RECEPTOR FOR PHORBOL ESTERS, A CLASS OF TUMOR PROMOTERS.
CC   -!- SIMILARITY: CONTAINS 2 ZINC DEPENDENT PHORBOL ESTER AND DAG
CC   BINDING DOMAINS.
CC   -!- SIMILARITY: CONTAINS 1 C2 DOMAIN.
CC   -!- SIMILARITY: [illegible]
CC   PKC SUBFAMILY.
CC   --
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CC   modified and this statement is not removed. Usage by and for commercial
CC   [illegible]
CC   or send an email to license@isb-sib.ch).
CC   --
DR   EMBL; X[illegible]; CAA[illegible]; -.
DR   PIR; S2[illegible]; S2[illegible].
DR   HSSP; P[illegible]; 1PTQ.
DR   MIM; [illegible]; -.
DR   InterPro; IPR00[illegible]; C2.
DR   InterPro; IPR002219; DAG_PE_bind.
DR   InterPro; IPR000719; Euk_pkinase.
DR   InterPro; IPR00[illegible]; Pkinase_C.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   Pfam; PF00168; C2; 1.
DR   Pfam; PF00130; DAG_PE-bind; 2.
DR   Pfam; PF00069; pkinase; 1.
DR   Pfam; PF00433; pkinase_C; 1.
DR   PRINTS; PR00[illegible]; [illegible].
DR   SMART; SM00[illegible]; C2; 1.
DR   SMART; SM00[illegible]; C1; 1.
DR   SMART; SM00133; S_TK_X; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   PROSITE; PS50004; C2_DOMAIN_2; 1.
DR   PROSITE; PS00479; DAG_PE_BIND_DOMAIN_1; 2.
DR   PROSITE; PS50081; DAG_PE_BIND_DOMAIN_2; 2.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW   Repeat; ATP-binding; Transferase; Phosphorylation;
KW   Serine/threonine-protein kinase; Phorbol-ester binding; Zinc.
FT   DOMAIN   1   99   C2 DOMAIN.
FT   DOMAIN   [illegible]   [illegible]   [illegible]
FT   DOMAIN   243   292   PHORBOL-ESTER AND DAG BINDING 2.
FT   DOMAIN   408   668   PROTEIN KINASE.
FT   NP_BIND   414   422   ATP (BY SIMILARITY).
FT   BINDING   437   437   ATP (BY SIMILARITY).
FT   ACT_SITE   532   532   BY SIMILARITY.
FT   MOD_RES   703   703   PHOSPHORYLATION (AUTO-) (POTENTIAL).
FT   MOD_RES   710   710   PHOSPHORYLATION (AUTO-) (POTENTIAL).
SQ   SEQUENCE   737 AA; 83673 MW; [illegible] CRC64;

  Query Match   5.6%; Score 167.[illegible]; DB [illegible]; Length 737;
  Best Local Similarity   23.2%; Pred. No. [illegible];
  Matches   76; Conservative   48; Mismatches 125; Indels   79; Gaps   15;

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Qy        1[illegible]2 KYELMKIENQ[illegible]EEELVLSWAL[illegible]                LLSCIHYIYEVIFATA 217
Db        421 KVMLAELKGKDE    VYAVKVLKKDV[illegible]                     ARKHHYLIQLY[illegible]FQ 477

Qy        218 NESSALLEMSNEGILKL[illegible]                                        [illegible]EVLE 27[illegible]
Db        478 TKDRLFFVMEYVNGG---DLMFQIQRS----RKFDEPRS        ----RFYAAEVISALM 521

Qy        278 FLHDKGFPYGHLHASNVMLDGD-PCKLLDL----  --      ENSLLGLPSFYRSYFSQF 324
Db        522 FLHQHGVIYRDLKLDNILLDAEGHCKLADFGMCKEGILNGVTTTTFCGTPDYIAPEILQ  580

Qy        325 EKINTLESVDVHSFGHLLYEMIYGKPP[illegible]       DSVEVDS -FFLAPSMAVVAVLE 372
Db        581 ELEYGPSVDWWALGVLMYEMMAGQ[illegible]                  KLAVSILE 6[illegible]

Qy        373 S---------TLSCPACKNCMP[illegible]          VL[illegible]SP KR[illegible]EKIPTKEKE     417
Db        6[illegible] AFNTKNPHKRLGCVA[illegible]QNGEDAIK      [illegible]WV[illegible]LE[illegible]                RRPVN 696

Qy        418                 ALKIAKE[illegible]EKRLIEE[illegible] 434
Db        697 NFDQDFTREEPVLTLVDEAIVKQINQEE 724
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RESULT 7
KPCE_MOUSE
ID   KPCE_MOUSE   STANDARD;   PRT;   737 AA.
AC   P16054;
DT   01-APR-1990 (Rel. 14, Created)
DT   01-APR-1990 (Rel. 14, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   Protein kinase C, epsilon type (EC 2.7.1.-) (NPKC-epsilon).
GN   PRKCE OR PKCE OR PKCEA.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=89137541; PubMed=291765[illegible];
RA   Schaap D., Parker P.J., Bristol A., Kriz R., Knopf J.;
RT   "Unique substrate specificity and regulatory properties of
RT   PKC-epsilon: a rationale for diversity.";
RL   FEBS Lett. 243:351-357(1989).
RN   [2]
RP   SEQUENCE FROM N.A.

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RC   [illegible] Brain.
RX   MEDLINE=[illegible]; PubMed=[illegible];
RA   Wang Q.J., Acs P., Goodnight J., Blumberg P.M., Mischak H.,
RA   Mushinski J.F.;
RT   "The catalytic domain of PKC epsilon, in reciprocal PKC delta and -
RT   epsilon chimeras, is responsible for conferring tumorgenicity to
RT   NIH3T3 cells, whereas both regulatory and catalytic domains of
RT   PKC epsilon contribute to in vitro transformation.";
RL   Oncogene 16:53-60(1998).
CC   -!- FUNCTION: THIS IS CALCIUM INDEPENDENT, PHOSPHOLIPID DEPENDENT,
CC       SERINE AND THREONINE SPECIFIC ENZYME.
CC   -!- FUNCTION: PKC IS ACTIVATED BY DIACYLGLYCEROL WHICH IN TURN
CC       PHOSPHORYLATES A RANGE OF CELLULAR PROTEINS. PKC ALSO SERVES AS
CC       THE RECEPTOR FOR PHORBOL ESTERS, A CLASS OF TUMOR PROMOTERS.
CC   -!- SIMILARITY: CONTAINS 2 ZINC DEPENDENT PHORBOL ESTER AND DAG
CC       BINDING DOMAINS.
CC   -!- SIMILARITY: CONTAINS 1 C2 DOMAIN.
CC   -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC       PKC SUBFAMILY.
CC   --------------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; AF[illegible]; AAB04[illegible].1; -.
DR   PIR; [illegible]; KIM[illegible].
DR   HSSP; [illegible]; [illegible].
DR   MGD; MGI:[illegible]; Prkce.
DR   InterPro; IPR[illegible]; C2.
DR   InterPro; IPR[illegible]; DAG_PE_bind.
DR   InterPro; IPR[illegible]; Euk_pkinase.
DR   InterPro; IPR[illegible]; Pkinase_C.
DR   InterPro; IPR[illegible]; Ser_thr_pkinase.
DR   Pfam; PF00168; C2; 1.
DR   Pfam; PF00130; DAG_PE-bind; 2.
DR   Pfam; PF00069; pkinase; 1.
DR   Pfam; PF00433; pkinase_C; 1.
DR   PRINTS; PR00008; DAGPEDOMAIN.
DR   SMART; SM00109; C1; 2.
DR   SMART; SM00239; C2; 1.
DR   SMART; SM00133; S_TK_X; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   PROSITE; PS50004; C2_DOMAIN_2; 1.
DR   PROSITE; PS00479; DAG_PE_BIND_DOM_1; 2.
DR   PROSITE; PS50081; DAG_PE_BIND_DOM_2; 2.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW   Repeat; ATP-binding; Transferase; Phosphorylation;
KW   Serine/threonine-protein kinase; Phorbol-ester binding; Zinc.
FT   DOMAIN        [illegible]    [illegible]       C2 DOMAIN.
FT   DOMAIN        [illegible]    [illegible]       PHORBOL ESTER AND DAG BINDING 1.
FT   DOMAIN        [illegible]    [illegible]       PHORBOL ESTER AND DAG BINDING 2.
FT   DOMAIN        [illegible]    [illegible]       PROTEIN KINASE.
FT   NP_BIND       4[illegible]    4[illegible]       ATP (BY SIMILARITY).
FT   BINDING       4[illegible]    4[illegible]       ATP (BY SIMILARITY).
FT   ACT_SITE      [illegible]    [illegible]       BY SIMILARITY.
FT   MOD_RES       [illegible]    [illegible]       PHOSPHORYLATION (AUTO-) (POTENTIAL).
FT   MOD_RES       [illegible]    [illegible]       PHOSPHORYLATION (AUTO-) (POTENTIAL).
SQ   SEQUENCE   737 AA;  [illegible] MW;  7AEBB[illegible]E57 CRC64;

  Query Match             5.5%;  Score 166.5;  DB 1;  Length 737;
  Best Local Similarity   23.2%;  Pred. No. 0.022;
  Matches   [illegible];  Conservative   [illegible];  Mismatches  125;  Indels   79;  Gaps   15;

Qy        1[illegible] KYEEMKIKN[illegible]LVLSWALG[illegible]KLQ[illegible]       [illegible]YYRVIFAFA 217
Db        1[illegible] KVMLAEL[illegible]    VYAVKVLKKDVIL[illegible]MTEKRILALA[illegible] 177

Qy        218 NE[illegible]AL[illegible]EMLNEK[illegible]KAK[illegible]NPKKIQ[illegible]EIY[illegible]EVLE 277
Db        478 FKDRLFFVMEYVNGG---DLMFQIQRS     RKFDEPRS            RFYAAEVISALM 521

Qy        278 FLHDKGFFYCHLHASNVMLDGD TCKL[illegible]            ENCL[illegible]YF[illegible]YISQF 324
Db        522 FLHQHGVIYRDLKLDNILLDAEGHCKLADFGMCKEGIMNGVTTTTFCGTPDYIAPEILQ 580

Qy        325 EKINT[illegible]VPVHCFGHLLYEMIYGKPP            [illegible]VPVH[illegible]  [illegible]AP[illegible]MAVVAVLE 372
Db        581  ELEYGPSVDWWALGVLMYEMMAGQPPFEADNEDDLFESILHDDVLYPVWLSKEAVSILK 639

Qy        373 S            [illegible]CEACKNGMP[illegible]   VI[illegible] KP[illegible]KLKF     417
Db        640 AFMTKNPHKRLGCVAAQNGEDAIK---QHPFFKEIDWVLLEQKKIKPPFKPRIKTKRDVN 696

Qy        418             ALKIAKD[illegible]IEKRLIEEQ 434
Db        697 NFDQDFTREEPILTLVDEAIIKQINQEE 724


RESULT 8
SNX6_HUMAN
ID   SNX6_HUMAN     STANDARD;      PRT;   343 AA.
AC   P57768;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Sorting nexin 16.
GN   SNX16.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Hanson B.J., Hong W.;
RL   Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: MAY BE INVOLVED IN SEVERAL STAGES OF INTRACELLULAR
CC       TRAFFICKING.
CC   -!- SIMILARITY: BELONGS TO THE SORTING NEXIN FAMILY.
CC   -!- SIMILARITY: CONTAINS 1 PHOX HOMOLOGY (PX) DOMAIN.
CC   --------------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; AF305779; AAG25676.1; -.
DR   InterPro; IPR001683; PX.
DR   Pfam; PF00787; PX; 1.
DR   SMART; SM00312; PX; 1.
KW   Transport; Protein transport; Coiled coil.
FT   DOMAIN      110    211       PX.
FT   DOMAIN      224    278       COILED COIL (POTENTIAL).
SQ   SEQUENCE   343 AA;  39153 MW;  EBE7229[illegible]BA46FF5 CRC64;

  Query Match             5.4%;  Score 161.5;  DB 1;  Length 343;
  Best Local Similarity   29.0%;  Pred. No. 0.016;
  Matches   51;  Conservative   29;  Mismatches   73;  Indels   23;  Gaps   [illegible];

Qy         17 IVPLIAAIEAGQSLQSHIIYIIEVQRGIGVENGWQIVKKYGDFDLLNNSLQ  TAGLSLP 74
Db        108 GIPTILSYEVMEERAKIVVKILVEK  IPEETWVVFKRYTDFVRLNDKLKEMFPGFRLA 16[illegible]

Qy         75 LLIKKLL  NKEKEFIAERQKTLQNYLNVLINHILNTDLVKEFL    [illegible]NNYSANYIF 1[illegible]
Db        1[illegible] LL[illegible]KWKR[illegible]NAL[illegible]KE[illegible]LA[illegible]VA[illegible]AN[illegible]LAVKEFLGLDDF          21[illegible]
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Qy        [illegible]VSMPERPEPKWPVV[illegible]KYFLMPIKNQPERRLV[illegible]WAPLSPL 186
Db        [illegible]

RESULT  [illegible]
SNXG_RAT
ID   SNX[illegible]_RAT      STANDARD;      PRT;   344 AA.
AC   [illegible]
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Sorting nexin 1[illegible]
GN   SNX1[illegible].
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=[illegible];
RN   [1]
RP   SEQUENCE FROM N.A.
RA   [illegible]
RL   Submitted ([illegible]) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: MAY BE INVOLVED IN SEVERAL STAGES OF INTRACELLULAR
CC       TRAFFICKING.
CC   -!- SIMILARITY: BELONGS TO THE SORTING NEXIN FAMILY.
CC   -!- SIMILARITY: CONTAINS 1 PHOX HOMOLOGY (PX) DOMAIN.
CC   --------------------------------------------------------------------------
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CC   entities requires a license agreement ([illegible])
CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; AF305[illegible]; AAG2567[illegible]; -.
DR   InterPro; IPR001683; PX.
DR   Pfam; [illegible]
DR   Pfam; [illegible]; PX; 1.
DR   SMART; SM00312; PX.
KW   Transport; Protein transport; Coiled coil.
FT   DOMAIN      [illegible]    [illegible]      PX.
FT   DOMAIN      [illegible]    278      COILED COIL (POTENTIAL).
SQ   SEQUENCE   344 AA;  [illegible]892 MW;  [illegible]2C22F CRC64;

  Query Match             5.[illegible]%;  Score 158.5;  DB 1;  Length 344;
  Best Local Similarity   30.[illegible]%;  Pred. No. 0.024;
  Matches   [illegible];  Conservative   27;  Mismatches   62;  Indels   17;  Gaps    6;

Qy        [illegible]
Db      108 SIP[illegible]CYEVMEEFAKFIVYF[illegible]VFF--[illegible]EFSWVVERRYTE[illegible]ELN[illegible]EEMFPGPRLA 165

Qy        [illegible]LPPKK[illegible]NM[illegible]NY[illegible]VKREL          [illegible]NNY 1[illegible]
Db      166 LPPKEWEKPNYNA[illegible]LEDRQL[illegible]QAILQNLVAHK[illegible]ANCLAVREFLCLD[illegible]PCPPDSLEE 225

Qy      1[illegible]5 SANV[illegible]PKWPVV[illegible] 1[illegible]
Db      226 S[illegible]EEINYHIQ[illegible]EVE[illegible]KEL 257

RESULT  [illegible]
PKPA_PHYBL
ID   PKPA_PHYBL     STANDARD;      PRT;   613 AA.
AC   Q0[illegible];
DT   15-[illegible]-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Serine/threonine protein kinase PKPA (EC 2.7.1.[illegible]).
GN   PKPA.
OS   Phycomyces blakesleeanus.
OC   Eukaryota; Fungi; Zygomycota; Zygomycetes; Mucorales; Mucoraceae;
OC   Phycomyces.
OX   NCBI_TaxID=4837;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=NRRL 1555;
RX   MEDLINE=96120859; PubMed=8590476;
RA   Ruiz Perez V.L., Murillo F.J., Torres Martinez S.;
RT   "PkpA, a novel Phycomyces blakesleeanus serine/threonine protein
RT   kinase.";
RL   Curr. Genet. 28:309-316(1995).
CC   -!- FUNCTION: SERINE/THREONINE PROTEIN KINASE THAT [illegible]
CC       PARTICIPATES AS AN INTERMEDIATE IN AN INTRACELLULAR SYSTEM
CC       CONTROLLING NUCLEAR PROLIFERATION.
CC   -!- DEVELOPMENTAL STAGE: MAINLY EXPRESSED DURING THE VEGETATIVE
CC       GROWTH, THE LEVEL DECREASED WHEN THE MYCELIUM CAN DIFFERENTIATE
CC       AND FORM SPORANGIOPHORES.
CC   -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
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CC   entities requires a license agreement ([illegible]/announce/
CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; Z46636; CAA86606.1; -.
DR   InterPro; IPR000719; Euk_pkinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   Pfam; PF00069; pkinase; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; FALSE NEG.
DR   PROSITE; [illegible]; PROTEIN_KINASE_ST; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW   Transferase; Serine/threonine-protein kinase; ATP-binding.
FT   DOMAIN       17    269       PROTEIN KINASE.
FT   NP_BIND      23     31       ATP (BY SIMILARITY).
FT   BINDING      50     50       ATP (BY SIMILARITY).
FT   ACT_SITE    140    140       BY SIMILARITY.
SQ   SEQUENCE   613 AA;  69594 MW;  [illegible]883[illegible] CRC64;

  Query Match             5.3%;  Score [illegible];  DB 1;  Length 613;
  Best Local Similarity   20.9%;  Pred. No. [illegible];
  Matches   99;  Conservative   65;  Mismatches  [illegible];  Indels  120;  Gaps   1[illegible];

Qy      192 KLP[illegible]LIKLL[illegible]LHPT[illegible]VIPA[illegible] N[illegible]ALL RMPNE[illegible]YRAKIKLPPLK 249
Db       57 KDLGHEIDILKSVKHPNI  ITFHDAWYNETEFVFITELMTSGILEEYIKKLTPLP 110

Qy        [illegible]
Db      111           NIKIVKKWTRQILKGLAYLHFRLEP[illegible]IHRD[illegible]KCPNIFINGAHGEIKIGD 159

Qy      [illegible]4 [illegible]LLEN [illegible]YRQYE[illegible]RF[illegible]Y[illegible]GRPP      [illegible]51
Db      160 MCTAEMKNGKKYTVIGTPEFMAPEMYEEQSYN  FKV[illegible]YAFGMC[illegible]LEMAIGEYPYGECT 217

Qy      [illegible]52 --------                 [illegible]VPVL[illegible]PA[illegible]MAVVAVLE[illegible]EA[illegible]KN[illegible]M [illegible]84
Db      218 NAVQVFKKVIQ[illegible]IKPECLSRVQDPEI[illegible]LVNIC[illegible]PEDDEM[illegible]AQEILSHRLL  AVEFEV 275

Qy      385 PIISRLLQMPLFS-DVLLTTSEK-  PQEKIF[illegible]KLKEA[illegible]EIAKD[illegible]IEKR IFFQKQ [illegible] 43[illegible]
Db      276 VLVS[illegible]DMTMK[illegible]LQVV[illegible]KGMDE[illegible]V[illegible]NA[illegible]AA[illegible]VVA[illegible]M[illegible]VE[illegible]N[illegible] YQQLITC 335

Qy      438 HQHRRLTRAQSHHGSEEERKKRK[illegible]LA[illegible]SK-KSALENS     ------------  475
Db      336 EINK[illegible]RD[illegible]ARNQGPPDKGKDEKIVW[illegible]N[illegible]EKRAKE[illegible]LALAVEKVFEAKKECELL 395

Qy      476 EEHG     AKYGNGNN[illegible]GA[illegible]PPPPPPPPAAP       526
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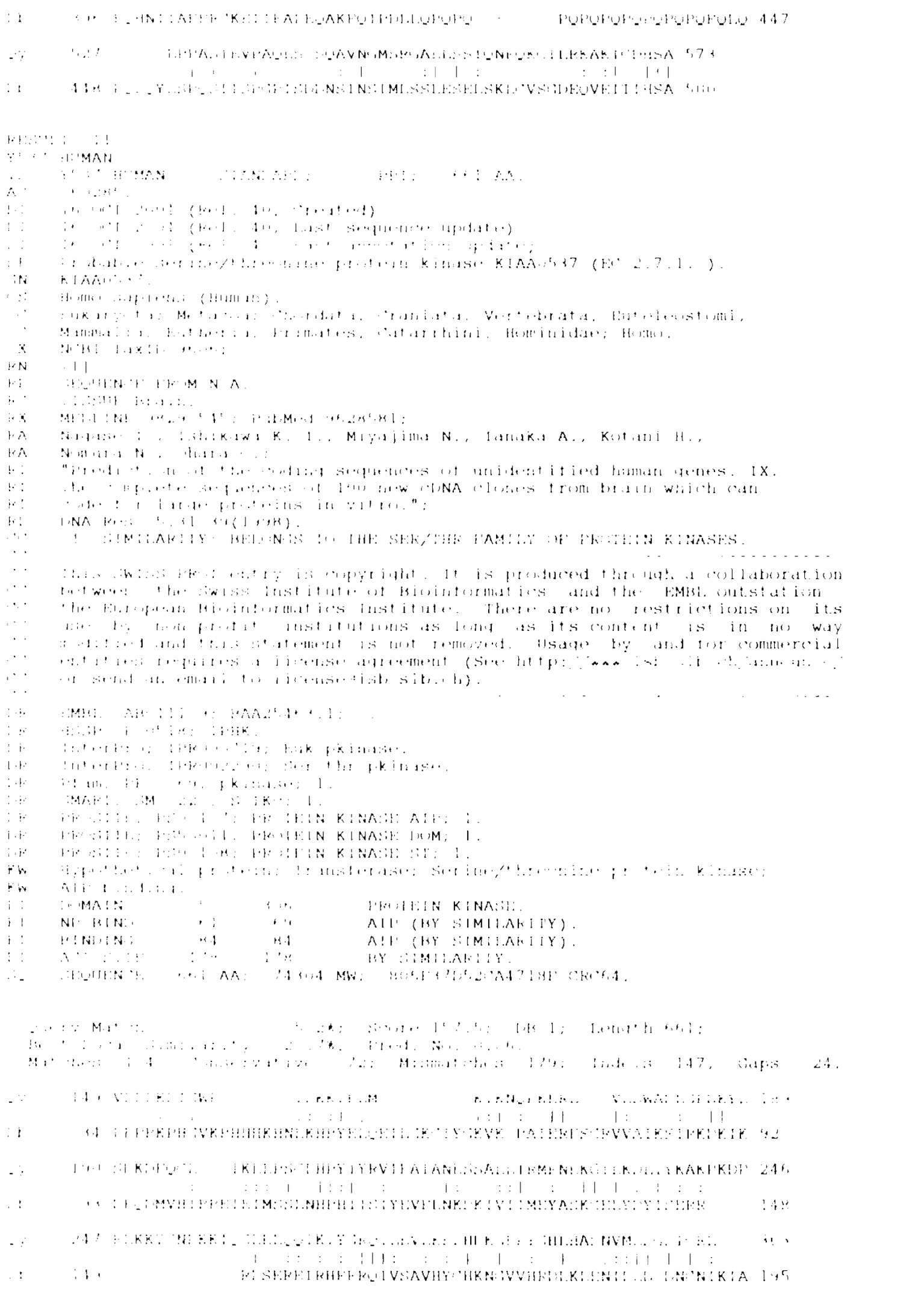

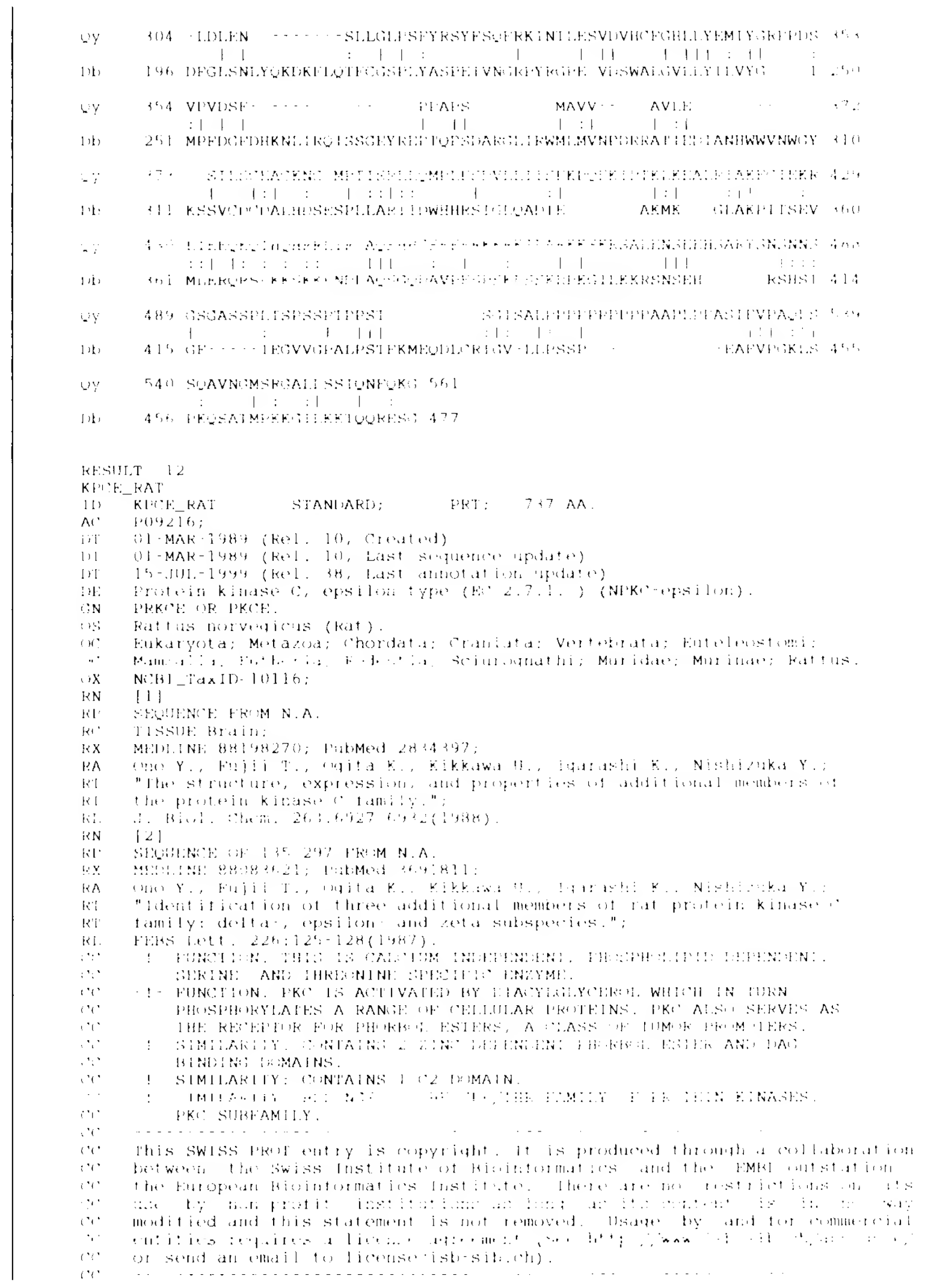

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DR   EMBL; M18331; AAA41872.1; -.
DR   PIR; B28143; KIRTCE.
DR   HSSP; P28867; 1PTQ.
DR   InterPro; IPR000008; C2.
DR   InterPro; IPR002219; DAG_PE-bind.
DR   InterPro; IPR000719; Euk_pkinase.
DR   InterPro; IPR000961; Pkinase_C.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   Pfam; PF00168; C2; 1.
DR   Pfam; PF00130; DAG_PE-bind; 2.
DR   Pfam; PF00069; pkinase; 1.
DR   Pfam; PF00433; pkinase_C; 1.
DR   PRINTS; PR00008; DAGPEDOMAIN.
DR   SMART; SM00109; C1; 2.
DR   SMART; SM00239; C2; 1.
DR   SMART; SM00133; S_TK_X;
DR   SMART; SM00220; S_TKc; 1.
DR   PROSITE; PS50004; C2_DOMAIN_2; 1.
DR   PROSITE; PS00479; DAG_PE_BIND_DOM_1; 2.
DR   PROSITE; PS50081; DAG_PE_BIND_DOM_2; 2.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW   Repeat; ATP-binding; Transferase; Phosphorylation;
KW   Serine/threonine-protein kinase; Phorbol-ester binding; Zinc.
FT   DOMAIN        1     99       C2 DOMAIN.
FT   DOMAIN       [illegible]    220       PHORBOL-ESTER AND DAG BINDING 1.
FT   DOMAIN      213    292       PHORBOL-ESTER AND DAG BINDING 2.
FT   DOMAIN      [illegible]    [illegible]       PROTEIN KINASE.
FT   NP_BIND     414    422       ATP (BY SIMILARITY).
FT   BINDING     437    437       ATP (BY SIMILARITY).
FT   ACT_SITE    532    532       BY SIMILARITY.
FT   MOD_RES     [illegible]    [illegible]       PHOSPHORYLATION (AUTO-) (POTENTIAL).
FT   MOD_RES     [illegible]    [illegible]       PHOSPHORYLATION (AUTO-) (POTENTIAL).
SQ   SEQUENCE   [illegible] AA;  [illegible] MW;  [illegible] CRC64;

  Query Match              5.1%;  Score 15[illegible]5;  DB 1;  Length 737;
  Best Local Similarity   22.9%;  Pred. No. 0.12;
  Matches   [illegible];  Conservative   47;  Mismatches  127;  Indels   79;  Gaps   15;

Qy        [illegible] KVMLAEKKGDE--VYAVKVLKKDVILQDDDVDCTMTEKRILALARKHPYLTQLYCCFQ 177
Db        [illegible] 

Qy        [illegible] IKEELFFVMEYVNGG--DLMFQIQRS---RKFDEPRS--------GFYAAEVTSALM 521
Db        

Qy        [illegible] ENSLLGLPGFYRSYPSQP 324
Db        [illegible] NGVTTTTFCGTPDYIAPEILQ- 580

Qy        [illegible] DSVPVDS- FPPAPSMAVVAVLE 372
Db        [illegible] KLAVGILK 639

Qy        [illegible] 417
Db        640 [illegible] VN 696

Qy        418 [illegible] ATRIAKECIEKRLIERQ 434
Db        [illegible]

RESULT 14
KPC4_DROME
ID   KPC4_DROME     STANDARD;      PRT;   511 AA.
AC   [illegible]VYN[illegible];
DT   01-MAR-2002 (Rel. 41, Created)
DT   01-MAR-2002 (Rel. 41, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
```

```
DE   Putative protein kinase C, delta type homolog (EC 2.7.1.-) (Fragment).
GN   Pkcdelta or CG10524.
OS   Drosophila melanogaster (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC   Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7227;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Berkeley;
RX   MEDLINE=20196006; PubMed=10731132;
RA   Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA   Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA   George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA   Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA   Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA   Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA   Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA   Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA   Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA   Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA   Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA   Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA   de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA   Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA   Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA   Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA   Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA   Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA   Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA   Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA   Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA   Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA   Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA   Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA   Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA   Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA   Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA   Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA   Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA   Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA   Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA   Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA   Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA   Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA   Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA   Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT   "The genome sequence of Drosophila melanogaster.";
RL   Science 287:2185-2195(2000).
RN   [2]
RP   CONCEPTUAL TRANSLATION.
RA   Manning G., Sudarsanam S., Plowman G.;
RT   "Prediction of novel protein kinases from the Drosophila genome
RT   project and EST sequences.";
RL   Unpublished observations (AUG-2000).
CC   -!- SIMILARITY: CONTAINS 2 ZINC FINGERS OF THE PHORBOL-ESTER/DAG
CC       BINDING DOMAINS.
CC   -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC       PKC SUBFAMILY.
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CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; AE003484; AAF48163.1; ALT_SEQ.
DR   FlyBase; FBgn0030487; Pkcdelta.
DR   HSSP; P28867; 1PTQ.
DR   InterPro; IPR002219; DAG_PE-bind.
DR   InterPro; IPR000719; Euk_pkinase.
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DR   InterPro; IPR[illegible]; Pkinase_C.
DR   InterPro; IPR[illegible]; Ser_thr_pkinase.
DR   InterPro; IPR[illegible]; Tyr_pkinase.
DR   Pfam; PF00130; DAG_PE-bind; 2.
DR   Pfam; PF[illegible]; pkinase; 1.
DR   Pfam; PF00433; pkinase_C; 1.
DR   PRINTS; PR00008; DAGPEDOMAIN.
DR   PRINTS; PR00109; TYRKINASE.
DR   SMART; SM00109; C1; 2.
DR   SMART; SM00220; S_TKc; 1.
DR   SMART; SM00133; S_TK_X; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00479; DAG_PE_BIND_DOM_1; 2.
DR   PROSITE; PS50081; DAG_PE_BIND_DOM_2; 2.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW   Hypothetical protein; ATP-binding; Transferase;
KW   Serine/threonine-protein kinase; Phorbol-ester binding; Metal-binding;
KW   Zinc; Repeat.
FT   NON_TER       1      1
FT   DOMAIN       15     65       PHORBOL ESTER AND DAG BINDING 1.
FT   DOMAIN       87    137       PHORBOL ESTER AND DAG BINDING 2.
FT   DOMAIN      1[illegible]    444       PROTEIN KINASE.
FT   NP_BIND     1[illegible]    2[illegible]       ATP (BY SIMILARITY).
FT   BINDING     215    215       ATP (BY SIMILARITY).
FT   ACT_SITE    [illegible]    [illegible]       BY SIMILARITY.
SQ   SEQUENCE   514 AA;  59422 MW;  39F9996D62AA497F CRC64;

  Query Match             5.1%;  Score 153;  DB 1;  Length 514;
  Best Local Similarity   24.5%;  Pred. No. 0.08;
  Matches   [illegible];  Conservative   37;  Mismatches  124;  Indels   70;  Gaps   13;

Qy        [illegible] KSLFQCE [illegible] KYLSGLRSLPLAANLLEEIALKNATLLELEMRPKRMLDSEIGLAS  248
Db        [illegible] [illegible]  273

Qy        [illegible] YKANLKDEELKNLNLHKLAEQESEKIEPIWYPEQTRALTGHLHPSHFLTWSTENIGPPTLHAFNVMELG  298
Db        274 [illegible]          ERARFYGAEIISGLKFLHKKGIIYRDLKLENVLLDY  320

Qy        [illegible]          [illegible] LENSLDGLPSEYRSYESQFRKINILESVDVHCFGILLYEM  345
Db        321 [illegible] YMAPEIIKGLKYN  QNVEWWGFGVLLYEM  378

Qy        346 [illegible]          VFVLGEFPAFGMAVVAVLEKGLSLRACKNGMLL[illegible]  383
Db        379 [illegible] NEIFWEVVIGAEAILLK[illegible]  436

Qy        384         RELLMELLSRVLLLLSEKPQFKIPIK         LKEALRIAKE[illegible]EKRLIE   432
Db        437 ALHIFFFPFDWGLLEKRQIEPPFKPQVKHPLDIQYFDRVFIRERVFLIP   IDKEILASM 496

Qy        433 RQKLIH 438

Db        497 [illegible]

RESULT 14
CR4_MAIZE
ID   CR4_MAIZE      STANDARD;      PRT;   901 AA.
AC   Q24585;
DT   15-DEC-1998 (Rel. 37, Created)
DT   15-DEC-1998 (Rel. 37, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   Putative receptor protein kinase CRINKLY4 precursor (EC 2.7.1.-).
GN   CR4
OS   Zea mays (Maize).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
OC   Panicoideae; Andropogoneae; Zea.
OX   NCBI_TaxID=4577;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CV. B73;
RX   MEDLINE=96355669; PubMed=8703079;
RA   Becraft P.W., Stinard P.S., McCarty D.R.;
RT   "CRINKLY4: A TNFR-like receptor kinase involved in maize epidermal
RT   differentiation.";
RL   Science 273:1406-1409(1996).
CC   -!- FUNCTION: PUTATIVE RECEPTOR PROTEIN KINASE. COULD PLAY A ROLE IN A
CC       DIFFERENTIATION SIGNAL. THE CRINKLY4 (CR4) MUTATION AFFECTS LEAF
CC       EPIDERMIS DIFFERENTIATION SUCH THAT CELL SIZE AND MORPHOLOGY ARE
CC       ALTERED, AND SURFACE FUNCTIONS ARE COMPROMISED, ALLOWING GRAFT
CC       LIKE FUSIONS BETWEEN ORGANS.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC   -!- SIMILARITY: CONTAINS A PARTIAL LA NGFR/TNFR TYPE CYSTEINE-RICH
CC       REGION.
CC   --------------------------------------------------------------------------
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CC   --------------------------------------------------------------------------
DR   EMBL; U67422; AAB09771.1; -.
DR   MaizeDB; 128723; -.
DR   InterPro; IPR000719; Euk_pkinase.
DR   InterPro; IPR004040; STY_pkinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00069; pkinase; 1.
DR   Pfam; PF00020; TNFR_c6; 1.
DR   SMART; SM00221; STYKc; 1.
DR   SMART; SM00208; TNFR; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00652; TNFR_NGFR_1; FALSE_NEG.
DR   PROSITE; PS50050; TNFR_NGFR_2; 1.
KW   Receptor; Transferase; Serine/threonine-protein kinase; ATP-binding;
KW   Repeat; Transmembrane; Signal.
FT   SIGNAL        1     24       POTENTIAL.
FT   CHAIN        25    901       PUTATIVE RECEPTOR PROTEIN KINASE
FT                                CRINKLY4.
FT   DOMAIN       25    423       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    424    444       POTENTIAL.
FT   DOMAIN      445    901       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       33    330       7 X 36 AA REPEATS.
FT   REPEAT       33     68       1.
FT   REPEAT       72    107       2.
FT   REPEAT      125    160       3.
FT   REPEAT      162    195       4.
FT   REPEAT      203    236       5.
FT   REPEAT      253    287       6.
FT   REPEAT      292    330       7.
FT   REPEAT      357    391       TNFR-CYS.
FT   DOMAIN      505    712       PROTEIN KINASE.
FT   NP_BIND     511    519       ATP (BY SIMILARITY).
FT   BINDING     533    533       ATP (BY SIMILARITY).
FT   ACT_SITE    634    634       BY SIMILARITY.
SQ   SEQUENCE   901 AA;  97439 MW;  52F8481AC187E061 CRC64;

  Query Match             5.1%;  Score 153;  DB 1;  Length 901;
  Best Local Similarity   20.1%;  Pred. No. 0.16;
  Matches  104;  Conservative   89;  Mismatches  192;  Indels  132;  Gaps   22;

Qy         78 EELLNNMKEEIAERQE[illegible]NYLNV [illegible]     NEILANTEIVEKFLENNYSANYIEIA 132
Db        415 RKIMAFQMKIEVALIVLAVVAVLAIVAVIALVAVRAKLRHC[illegible]SNR           FLK 462
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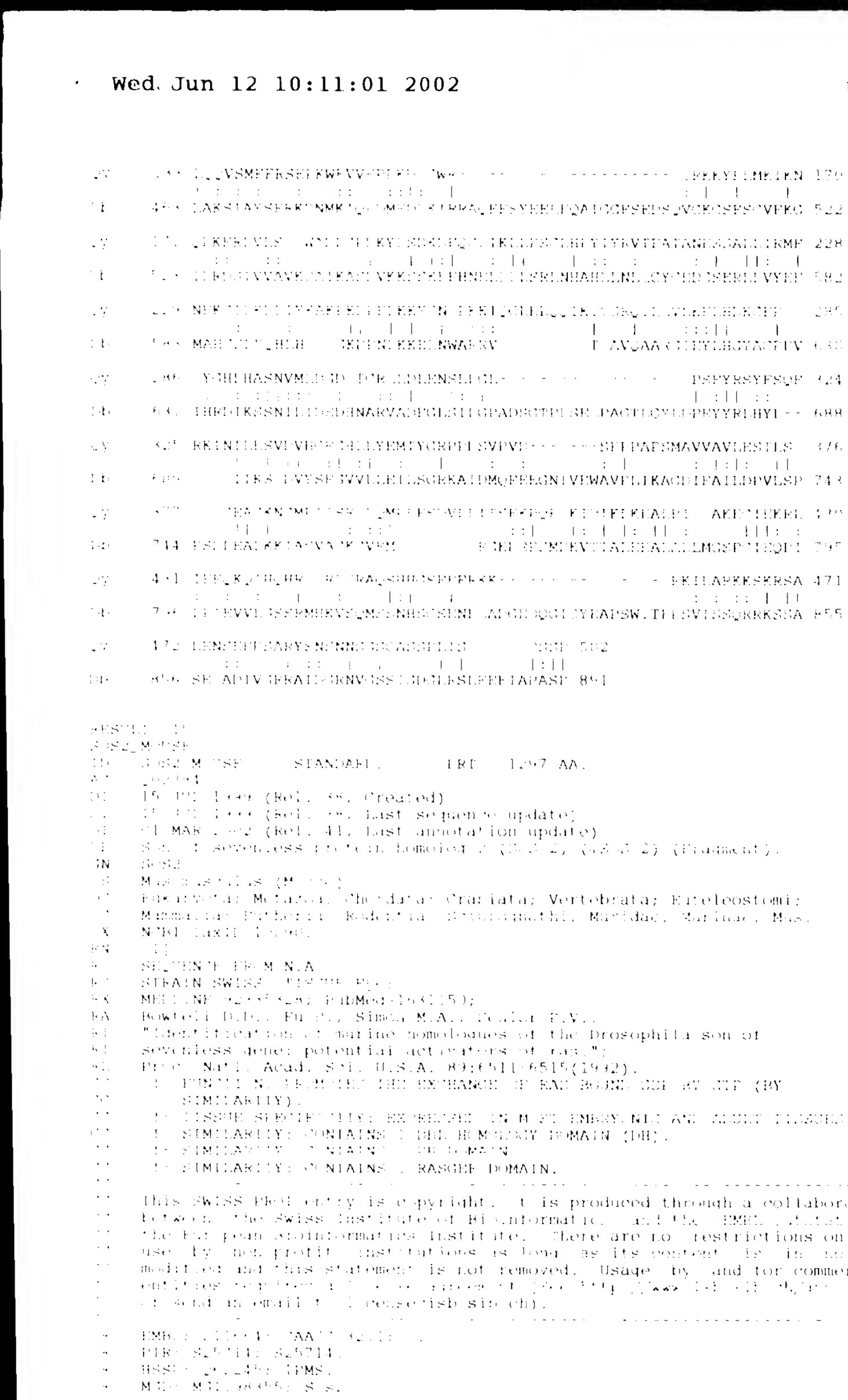

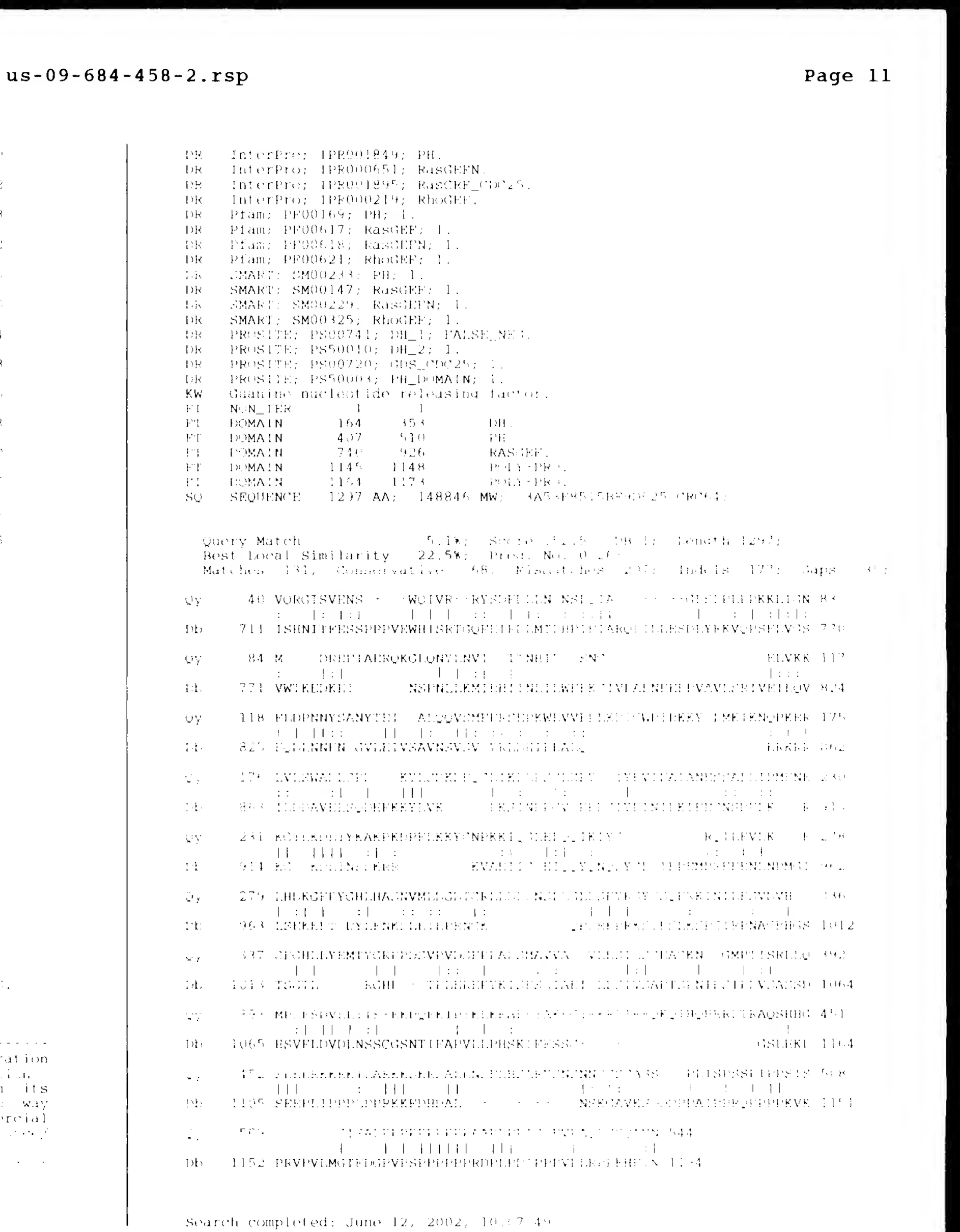

OM protein - protein search, using sw model

Run on: June 12, 2002, 09:53:49 ; Search time 94.83 Seconds
(without alignments)
584.663 Million cell updates/sec

Title: US-09-684-458-2
Perfect score: 3001
Sequence: 1 MAEMEKPPACRVLLDDVI..........PQKGILRKAKICDHSAPKIG 577

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	195	6.5	1081	2	S51899	probable protein k
2	182	6.1	1851	2	T19964	hypothetical prote
3	171.5	5.7	1228	2	T18892	hypothetical prote
4	170.5	5.7	895	2	T15881	hypothetical prote
5	168.5	5.6	736	1	KIRBCE	protein kinase C (
6	167.5	5.6	737	1	S28942	protein kinase C (
7	165.5	5.5	737	1	KIMSCE	protein kinase C (
8	160	5.3	633	1	S49011	probable serine/th
9	158.5	5.3	1032	2	D83037	serine/threonine p
10	158	5.3	1206	2	T34021	protein kinase SK2
11	158	5.3	[illegible]	2	T18932	serine/threonine pr
12	155.5	5.2	1233	2	T14157	serine/threonine p
13	154.5	5.1	967	2	E96636	hypothetical prote
14	153.5	5.1	737	1	KIRTCE	protein kinase C (
15	153.5	5.1	1621	2	T15264	hypothetical prote
16	153	5.1	576	2	T36729	probable serine/th
17	153	5.1	941	2	T34108	receptor kinase ho
18	152.5	5.1	1297	2	S25714	son of sevenless 2
19	151.5	5.0	1466	1	EDBEIF	immediate-early pr
20	149.5	5.0	1260	1	TVFINU	protein-tyrosine k
21	149	5.0	676	1	S35704	protein kinase C (
22	149	5.0	1087	2	T16511	hypothetical prote
23	147.5	4.9	834	2	T09512	serine/threonine s
24	144	4.8	1255	1	A24571	protein-tyrosine k
25	143.5	4.8	512	2	T47733	receptor-like prot
26	143.5	4.8	1794	2	T38459	hypothetical diver
27	143	4.8	442	2	[illegible]	[illegible]
28	142	4.7	426	2	S71886	Ste20-like protein
29	142	4.7	820	2	T09645	hypothetical prote
30	142	4.7	1585	2	T31611	hypothetical prote
31	141	4.7	433	2	T46512	probable serine/th
32	141	4.7	1064	2	T13993	termin related pro
33	140	4.7	505	1	S77034	protein kinase pkn
34	140	4.7	982	2	T18576	serine threonine k
35	139	4.6	674	1	KIMSCD	protein kinase C (
36	138.5	4.6	613	2	T15489	hypothetical prote
37	138.5	4.6	981	1	FOMVAM	gag-abl polyprotei
38	138.5	4.6	1375	2	S48005	hypothetical prote
39	137.5	4.6	842	2	S60452	protein kinase CLA
40	137.5	4.6	1271	2	S37958	myosin heavy chain
41	137	4.6	304	2	H86302	12082.26 protein
42	137	4.6	673	1	KIRBCT	protein kinase C (
43	137	4.6	939	2	S28034	probable serine/th
44	137	4.6	1254	2	T48101	p185 precursor
45	137	4.6	1737	2	A59255	unconventional myo

ALIGNMENTS

RESULT 1
S51899
probable protein kinase HRC1081 (EC 2.7.1.-) - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein O0784; protein YOL100w
C;Species: Saccharomyces cerevisiae
C;Date: 05-May-1995 #sequence_revision 18-Aug-1995 #text_change 24-Sep-1999
C;Accession: S51899; S59175; S66796
R;Vandenbol, M.; Durand, P.; Portetelle, D.; Hilger, F.
submitted to the EMBL Data Library, January 1995
A;Description: Sequence analysis of a 44kb DNA fragment of yeast chromosome XV includ
and a Delta.
A;Reference number: S51848
A;Accession: S51899
A;Molecule type: DNA
A;Residues: 1-1081 <VAN>
A;Cross-references: EMBL:Z48149; NID:g663234; PIDN:CAA88162.1; PID:g663254
R;Vandenbol, M.; Durand, P.; Portetelle, D.; Hilger, F.
Yeast 11, 1069-1075, 1995
A;Title: Sequence analysis of a 44 kb DNA fragment of yeast chromosome XV including
a delta element.
A;Reference number: S59156; MUID:96077[illegible]
A;Accession: S59175
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-1081 <VAW>
A;Cross-references: EMBL:Z48149; NID:g663234; PIDN:CAA88162.1; PID:g663254
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1995
R;Durand, P.; Hilger, F.; Portetelle, D.; Vandenbol, M.
submitted to the Protein Sequence Database, July 1995
A;Reference number: S66791
A;Accession: S66796
A;Molecule type: DNA
A;Residues: 1-1081 <DUR>
A;Cross-references: EMBL:Z74842; NID:g1419[illegible]; PIDN:CAA99[illegible]; PID:g251892; PID:g14[illegible]
A;Experimental source: strain S288C
C;Genetics:
A;Map position: 15L
C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase hom
C;Keywords: ATP; phosphotransferase
F;177-443/Domain: protein kinase homology <KIN>
F;185-193/Region: protein kinase ATP-binding motif

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  Query Match             6.5%;  Score 195;  DB 2;  Length 1081;
  Best Local Similarity   21.4%;  Pred. No. [illegible];
  Matches  [illegible];  Conservative   74;  Mismatches  [illegible];  Indels  144;  Gaps  [illegible];

Qy        161 EEYFLMKIENQPEERLVLSWAP[illegible]ANES 220
              [illegible]
Db        212 FEEYAAFVLN  FFYLIFL    [illegible]SIFQDES 2[illegible]

Qy        221 [illegible]
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Db    [illegible] YAENE[illegible]MKKY[illegible]LDEICARY          ---YAAQ[illegible]DAIDYLH 295

Qy    [illegible] HASNVM[illegible]          [illegible]RLLDLENSL[illegible]LPSFYRSYF[illegible]RKINILE 331

Db    [illegible] EMKIKLIDFCIAKLLNPINNSVSKPEYDLSIRSK SFVGIAE 354

Qy    [illegible] DV          [illegible]VH[illegible]FGHLLYEMIYGRPPDSVPVD          SFPPAPSM 365

Db    [illegible] YV[illegible]IWAP[illegible]LFQMIAGKP[illegible]KAINEYLTFQKVMKVQYAPIPGFPL 414

Qy    366 AVVAV[illegible]GMP[illegible]ISRLLQMPLESDVLL -------TISEKPQFKIPTKL 415

Db    415 [illegible]LVKKIL     VKNL[illegible]LISQIK[illegible]FKDLNF[illegible]SVWSKIP[illegible]KPYKINAKS 470

Qy    416 KEAL          RIAKE[illegible]I     EKRLIEEQK     -QIHQHRRLTRAQSHH[illegible]SEEERKKR 459

Db    471 M[illegible]AM[illegible]KIVK[illegible]VN[illegible]LVIQ[illegible]ASSPSVEEIIHSILYNNNIBASIESEISIK 530

Qy    460 K[illegible]ARKKSKKSA  LEN          -    SEFHSARYSNSN 486

Db    531 K    [illegible]DERIAQ[illegible]LENA[illegible]NN[illegible]EN[illegible]AA[illegible]AALAA[illegible]AAL[illegible]EEIM[illegible]SYPL[illegible] 587

Qy    487 N[illegible]ASSPLI[illegible]          PSSPTPP STSGISALPPPPPPPPPPAAPLPPA 530

Db    588 [illegible]AI[illegible]YKKI[illegible]AKS[illegible]ASVL[illegible]SKV[illegible]MPPYI[illegible]MS[illegible]MIPY 647

Qy    [illegible]

Db    [illegible]
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RESULT 2
I[illegible]4
hypothetical protein C46C2.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: [illegible]
R;McMurray, A.
submitted to the EMBL Data Library, December 1995
A;Reference number: Z[illegible]
A;Accession: [illegible]
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1851 <WIL>
A;Cross-references: EMBL:Z68296; PIDN:CAA92591.1; GSPDB:GN00022; CESP:C46C2.1
A;Experimental source: clone C46C2
C;Genetics:
A;Gene: CESP:C46C2.1
A;Map position: 4
A;Introns: [illegible]

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  Best Local Similarity   22.2%;  Pred. No. 0.028;
  Matches  10[illegible];  Conservative   61;  Mismatches  160;  Indels  146;  Gaps   22;

Qy    176 LVLSWADLGPDKY  LSDKDFQCLIKLLPSCLHPYIYRVIFATANESSAL   ------LI 225

Db    368 VAVAW[illegible]LNKIEPQ[illegible]AEMLEDLQHPNIVK  FYDYWESAD[illegible]CKKKYIVLV 425

Qy    226 KMENEKC[illegible]YEAK[illegible]KKY   CNPKK[illegible]QIKIYGRQILEVLKFLHDKG 283

Db    426 TELMISGTLK          MYLKPEEKRINIEVV     LKSW[illegible]RQIL[illegible]CLSFLHTRN 468

Qy    284 FFYGH  LHASNVML[illegible]          [illegible]RLLDLEN     [illegible]LPSF     YRSYFSQF 324

Db    469 P[illegible]VIHRDLK[illegible]DNIF[illegible]VKI[illegible]LATLKNKSFAKSVIGTPEFMAPEMYEEMYD-  526

Qy    325 RKINILESVDVH[illegible]FGHLLYEMIYGRPPDS          -  VPVDSFP  PAPSMAV 367

Db    527        [illegible]SVDVYAF[illegible]M[illegible]LEMV[illegible]GEYPY[illegible]MNPA[illegible]KVISGVKP[illegible]SKIPAQYPEI 580

Qy    368 VAVLESTLSCEACKNGMPTISRLLQMPLESD     -          VLL 401

Db    581 KEIIDRCIRVR  RKERSTVKQLLVHDPF[illegible]IRVEIKNRPARLNELNVE[illegible]MQLR 638

Qy    402 TISEKPQFKIPIKLKEALRIAKE[illegible]          IEKRLIEEQ          434

Db    639 VYD[illegible]ENE[illegible]QFAE[illegible]NDS[illegible]VV[illegible]QMI[illegible]M[illegible]VDA 698

Qy    435 KQIHQHRRLIRAQSHH[illegible]ARK[illegible]NSEEHSARYSNSNNSGSGAS 493

Db    699 FRKDRDHRLL---EIKPAKE[illegible]IRKEAF[illegible]AEAK[illegible]EKRLEEEKLEEFAAA 755

Qy    494 SPLTSPSSPTPPSTSGISALPPPPPPPPPPA -APL-PPASIEVPAQLSSQA 542

Db    756 AAAANP NPTP          IPPIPATPHSSAQQQPIPPPLSIQISAEIQQSA 798
```

RESULT 3
I18897
hypothetical protein C04A11.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: [illegible] #sequence_revision [illegible] #text_change 18-Feb-2000
C;Accession: I18897
R;McMurray, A.
submitted to the EMBL Data Library, November 1996
A;Reference number: Z19041
A;Accession: I18897
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1228 <WIL>
A;Cross-references: EMBL:Z81460; PIDN:CAB03829.1; GSPDB:GN00028; CESP:C04A11.3
A;Experimental source: clone C04A11
C;Genetics:
A;Gene: CESP:C04A11.3
A;Map position: X
A;Introns: [illegible]

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  Query Match             5.7%;  Score 171.5;  DB 2;  Length 1228;
  Best Local Similarity   22.2%;  Pred. No. 0.063;
  Matches  113;  Conservative   63;  Mismatches  188;  Indels  145;  Gaps   22;

Qy    1[illegible] NNDSANY[illegible]    F[illegible]  M[illegible] 169

Db      9 NLFRANQA[illegible]YDNVN[illegible]WN[illegible]AA[illegible]SIE 67

Qy    170 NQPKFRLVLSWADLGPDKYLSDKDFQCLIKLLPSCL HPYIYRVIFATANESSALLIRMF 228

Db     68 IQEGEEL          EDFLVEIEI[illegible]SD[illegible]KGHPVML[illegible]YSIYFFENKLIMLLEF 112

Qy    2[illegible] [illegible]FFYGH 288

Db    113 CGGGAVDNIIVELG          HVLKEDQIRYIGYYVCDALKWLHSQNVIHRD 157

Qy    289 LHASNVMLDGD [illegible]RLLDL          EN[illegible]LGLPSFYRSYF[illegible]KINI[illegible]SV - 333

Db    158 LKACN[illegible]VELADF[illegible]SAKLKS[illegible]     -- YWMA[illegible]VMA[illegible] 211

Qy    334 -------DVHCFGHLLYEMIYGRPPDSVPVDSFPPAPSMAVVAVLESTLSCEACKNGMPT 386

Db    212 QPYDCISDIWSFGIILIEMAQGEPPHS----------DVSVMRVI-----IKVQKSEPPT 256

Qy    387 ISRLLQ----MPLFSDVLLITSEK-PQFKIPTKLKEALRIAKECIEKRLIEEQKQIHQHR 441

Db    257 --LLQPSHWIRSFSDIILRCLVKDPRNRPPA-   -          --  AKIFKHQ 292

Qy    442 R[illegible]KAQ[illegible]          [illegible]ARYSNSNN 487

Db    293 WFQNAPS-  -   - KKKMIMDLLAEMYADVQEEVVIDGDEESVAGSDEISQRRGDSWS 343

Qy    488 SGSGASSPLISPSSPTPPSTSGISALPPPPPPPPPPAAPLPPASTEVPAQLSSQAVNGMS 547

Db    344 SASDSPRPAISDGFKVPIVSVPIIETPPPIIPHKKRAAPPPP- QEVNAHRQSPVVNG  399
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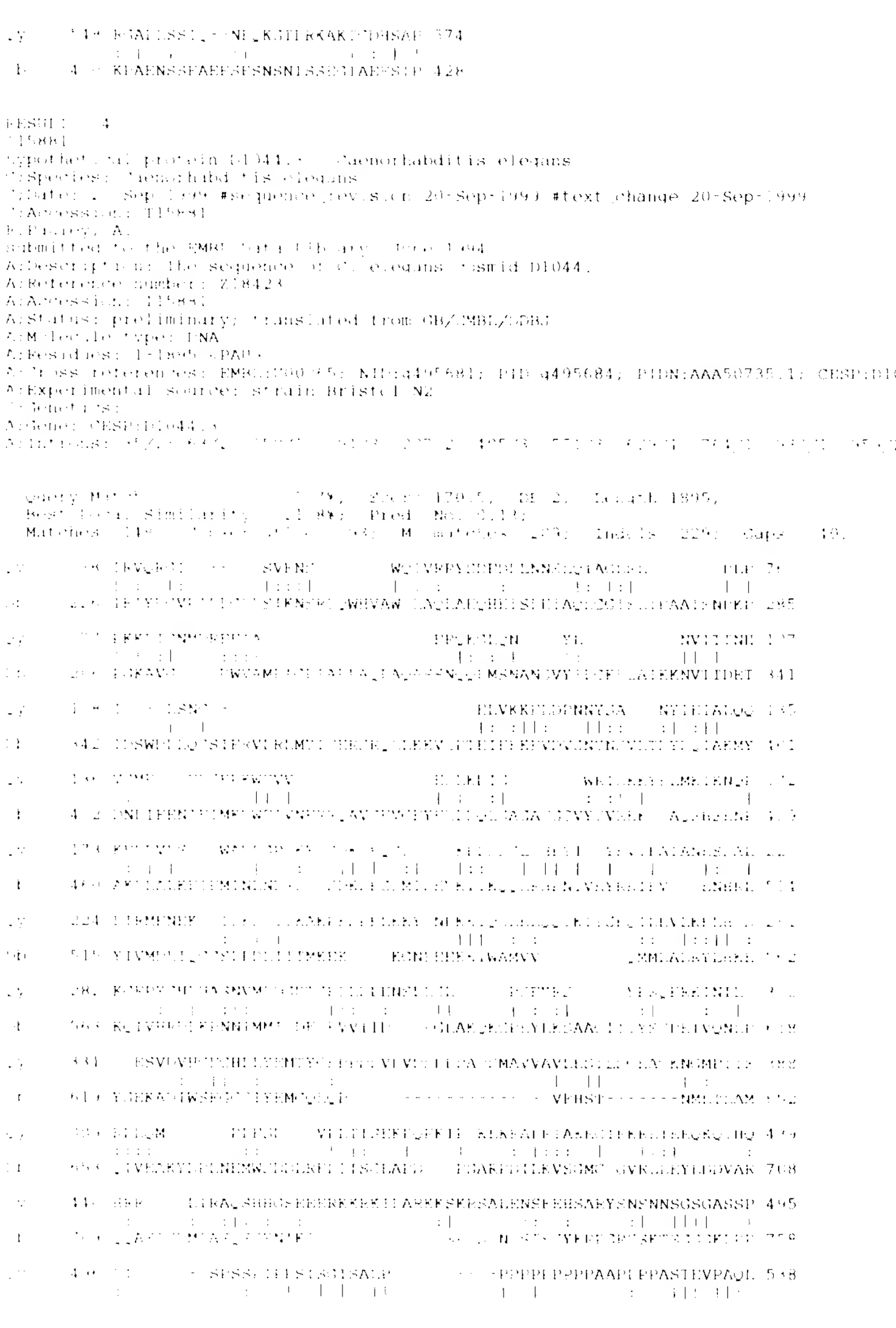

RESULT 4
D1044
hypothetical protein D1044.x - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 2-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Accession: D1044
R;Barrey, A.
Submitted to the EMBL Data Library, Dec 1994
A;Description: The sequence of C. elegans cosmid D1044.
A;Reference number: Z28423
A;Accession: D1044
A;Status: preliminary; translated from GB/EMBL/GSDB
A;Molecule type: DNA
A;Residues: 1-1065 <PAR>
A;Cross-references: EMBL:Z90475; NID:g495681; PID:g495684; PIDN:AAA50735.1; CESP:D1044.3
A;Experimental source: strain: Bristol N2
C;Genetics:
A;Gene: CESP:D1044.x
A;Map position: [illegible]

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Best Local Similarity [illegible]; Pred. No. 0.13;
Matches [illegible]; Conservative [illegible]; Mismatches [illegible]; Indels [illegible]; Gaps [illegible].

RESULT 5
KIRBOE
protein kinase C (EC 2.7.1.-) epsilon - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 21-Nov-1997
C;Accession: A29880
R;Ohno, S.; Akita, Y.; Konno, Y.; Imajoh, S.; Suzuki, K.
Cell 53, 731-741, 1988
A;Title: A novel phorbol ester receptor/protein kinase, nPKC, distantly related [illegible]
A;Reference number: A29880; MUID:88222467
A;Accession: A29880
A;Molecule type: mRNA
A;Residues: 1-736 <OHN>
A;Cross-references: GB:M20014
C;Function:
A;Description: catalyzes the formation of peptidyl serine phosphate or peptidyl [illegible]
A;Note: activity is calcium independent, phospholipid dependent, and activated by di[illegible]
C;Superfamily: protein kinase C; protein kinase C zinc binding repeat homology
C;Keywords: ATP; autophosphorylation; diglyceride; phorbol ester binding; phospho[illegible]
F;156-161/Region: pseudophosphorylation motif
F;170-220/Domain: protein kinase C zinc-binding repeat homology #827>
F;212-262/Domain: protein kinase C zinc-binding repeat homology #872>
F;185-667/Domain: protein kinase homology #1>
F;413-421/Region: protein kinase A/C binding motif
F;176,201,204,220/Binding site: zinc (his, cys, cys, cys) #status predicted
F;184,186,209,212/Binding site: zinc (cys, cys, his, cys) #status predicted
F;217,224,227,242/Binding site: zinc (his, cys, cys, cys) #status predicted
F;256,259,281,284/Binding site: zinc (cys, cys, his, cys) #status predicted
F;136,155,531,533/Active site: lys, Glu, Asp, lys #status predicted
F;702,709/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status [illegible]

Query Match [illegible]; Score [illegible]; DB [illegible]; Length 736;
Best Local Similarity [illegible]; Pred. No. [illegible];
Matches [illegible]; Conservative [illegible]; Mismatches [illegible]; Indels [illegible]; Gaps [illegible];

RESULT 6
J03944
protein kinase C (EC 2.7.1.) epsilon [illegible]
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jun-1999

```
C;Accession: S28042
R;Basta, P.; Strickland, M.B.; Holmes, W.; Loomis, C.R.; Ballas, L.M.; Burns, D.J.
Biochim. Biophys. Acta 1132, 154-160, 1992
A;Title: Sequence and expression of human protein kinase C-epsilon.
A;Reference number: S28042; MUID:93003318
A;Accession: S28042
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-737 <BAS>
A;Cross-references: EMBL:X65293; NID:g35494; PIDN:CAA46389.1; PID:g35495
C;Comment: This is a calcium independent, phospholipid dependent, serine- and threonine-
 of neutral phospholipids. This protein is a receptor for tumor promoting phorbol ester
C;Genetics:
A;Gene: GDB:PRKCE
A;Cross-references: GDB:128039; OMIM:176975
A;Map position: [illegible]
C;Function:
A;Description: catalyzes the formation of peptidyl serine phosphate or peptidyl threonin
A;Note: activity is calcium independent, phospholipid dependent, and activated by diacyl
C;Superfamily: protein kinase C delta; protein kinase C zinc binding repeat homology; pr
C;Keywords: ATP; duplication; phorbol ester binding; phospholipid binding; phosphotransf
F;156-161/Region: pseudophosphorylation motif
F;170-220/Domain: protein kinase C zinc binding repeat homology <KZ1>
F;243-292/Domain: protein kinase C zinc binding repeat homology <KZ2>
F;406-668/Domain: protein kinase homology <KIN>
F;414-422/Region: protein kinase ATP binding motif
F;170,201,204,220/Binding site: zinc (His, Cys, Cys, Cys) #status predicted
F;183,186,205,212/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
F;243,273,276,292/Binding site: zinc (His, Cys, Cys, Cys) #status predicted
F;256,259,281,284/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
F;437,456,532,534/Active site: Lys, Glu, Asp, Lys #status predicted

  Query Match             5.6%;  Score 167.5;  DB 1;  Length 737;
  Best Local Similarity   23.2%;  Pred. No. 0.056;
  Matches   76;  Conservative   48;  Mismatches  125;  Indels   79;  Gaps   15;

Qy        162 KYFLMKIKNQPKKRLVLSWAPKTPPKYLSPKPPQCLIK    LLLPSCLHPYIYRVIEATA 217
Db        421 KVMLAELKGKDE   VYAVKVLKKDVILQDDDVDCTMTEKRILALARKHPYLTQLYCCFQ 477

Qy        218 NLSSALLIEMLNEKGTLEELLIKKAPPKGTLEKY NEKKTQGLLLQQLRTYLRQLLLVLK 277
Db        478 TKDRLFFVMEYVNGG   DLMFQIQRS     RKFDEPRS             RFYAAEVISALM 521

Qy        278 FLHEKGFPYGHLHASNVMLDGD TPKLLDL                   ENSLLGLPSFYRSYFSQF 324
Db        522 FLHQHGVIYRDLKLDNILLDAEGHCKLADFGMCKEGILNGVTTTTFCGTPDYIAPEILQ  580

Qy        325 RKINTLLEGVLVHTFGHLLYEMIYGRPP              DSVPVDS   FPPAPSMAVVAVLE 372
Db        581  ELEYGPSVDWWALGVLMYEMMAGQPPFEADNEDDLFESILHDDVLYPVWLSKEAVSILK 639

Qy        373 S              LLSTEACKNGMPTISRLLQMPLFSD   VLLIISE KPQEKIPIKIKE   417
Db        640 AFMTKNPHKRLGCVAAQNGEDAIK    QHPFFKEIDWVLLEQKKIKPPFKPRIKTKRDVN 696

Qy        418             ALRIAKECIEKRLIEEQ 434
Db        697 NFDQDFTREEPVLTLVDEAIVKQINQEE 724


RESULT    7
KIMSCE
protein kinase C (EC 2.7.1.-) epsilon - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1991 #sequence_revision [illegible] Sep 1992 #text_change 21 Nov 1997
C;Accession: S02227
R;Schaap, D.; Parker, P.J.; Bristol, A.; Kriz, R.; Knopf, J.
FEBS Lett. 243, 351-357, 1989
A;Title: Unique substrate specificity and regulatory properties of PKC-epsilon: a ration
A;Reference number: S02226; MUID:89137541
A;Accession: S02226
A;Status: nucleic acid sequence not shown, not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-737 <SCH>
C;Function:
A;Description: catalyzes the formation of peptidyl serine phosphate or peptidyl threo
A;Note: activity is calcium-independent, phospholipid dependent, and activated by dia
C;Superfamily: protein kinase C delta; protein kinase C zinc binding repeat homology;
C;Keywords: ATP; autophosphorylation; duplication; phorbol ester binding; phospholipi
F;156-161/Region: pseudophosphorylation motif
F;170-220/Domain: protein kinase C zinc binding repeat homology <KZ1>
F;243-292/Domain: protein kinase C zinc binding repeat homology <KZ2>
F;406-668/Domain: protein kinase homology <KIN>
F;414-422/Region: protein kinase ATP binding motif
F;170,201,204,220/Binding site: zinc (His, Cys, Cys, Cys) #status predicted
F;183,186,205,212/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
F;243,273,276,292/Binding site: zinc (His, Cys, Cys, Cys) #status predicted
F;256,259,281,284/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
F;437,456,532,534/Active site: Lys, Glu, Asp, Lys #status predicted
F;703,710/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status p

  Query Match             5.5%;  Score 166.5;  DB 1;  Length 737;
  Best Local Similarity   23.2%;  Pred. No. 0.062;
  Matches   76;  Conservative   48;  Mismatches  125;  Indels   79;  Gaps   15;

Qy        162 KYFLMKIKNQPKKRLVLSWAPKTPPKYLSPKPPQCLIK-    LLLPSCLHPYIYRVIEATA 217
Db        421 KVMLAELKGKDE---VYAVKVLKKDVILQDDDVDCTMTEKRILALARKHPYLTQLYCCFQ 477

Qy        218 NLSSALLIEMLNEKGTLEELLIKKAPPKGTLEKYNEKKTQGLLLQQLRTYLRQLLLVLK 277
Db        478 TKDRLFFVMEYVNGG--DLMFQIQRS-    RKFDEPRS             RFYAAEVISALM 521

Qy        278 FLHEKGFPYGHLHASNVMLDGD TPKLLDL--  ----  -    ENSLLGLPSFYRSYFSQF 324
Db        522 FLHQHGVIYRDLKLDNILLDAEGHCKLADFGMCKEGILNGVTTTTFCGTPDYIAPEILQ  580

Qy        325 RKINTLLEGVLVHTFGHLLYEMIYGRPP              DSVPVDS   FPPAPSMAVVAVLE 372
Db        581  ELEYGPSVDWWALGVLMYEMMAGQPPFEADNEDDLFESILHDDVLYPVWLSKEAVSILK 639

Qy        373 S              LLSTEACKNGMPTISRLLQMPLFSD    VLLIISE KPQEKIPIKIKE   417
Db        640 AFMTKNPHKRLGCVAAQNGEDAIK---QHPFFKEIDWVLLEQKKIKPPFKPRIKTKRDVN 696

Qy        418 ------------ALRIAKECIEKRLIEEQ 434
Db        697 NFDQDFTREEPVLTLVDEAIVKQINQEE 724


RESULT    8
S49611
probable serine/threonine-specific protein kinase pkpA (EC 2.7.1.-) - Phycomyces blak
C;Species: Phycomyces blakesleeanus
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: S49611; S59578
R;Ruiz Perez, V.; Murillo, F.; Torres-Martinez, S.
submitted to the EMBL Data Library, November 1994
A;Description: A novel serine/threonine protein kinase in the fungus Phycomyces blake
A;Reference number: S49611
A;Accession: S49611
A;Molecule type: DNA
A;Residues: 1-633 <RUI>
A;Cross-references: EMBL:Z46636
R;Ruiz Perez, V.L.; Murillo, F.J.; Torres-Martinez, S.
Curr. Genet. 28, 309-316, 1995
A;Title: PkpA, a novel Phycomyces blakesleeanus serine/threonine protein kinase.
A;Reference number: S59578; MUID:96120859
A;Accession: S59578
A;Molecule type: DNA
A;Residues: 1-9;39-346 <RUW>
A;Cross-references: EMBL:Z46636
A;Note: only part of the coding region is given
```

C;Genetics:
A;Gene: pkpA
A;Introns: [illegible]
C;Superfamily: Phycomyces blakesleeanus probable serine/threonine specific protein kinas
C;Keywords: phosphotransferase; protein kinase
F;34-[illegible]/Domain: protein kinase homology <KIN>

Query Match [illegible]; Score 63; DB 1; Length 633;
Best Local Similarity [illegible]; Pred. No. 0.12;
Matches [illegible]; Conservative [illegible]; Mismatches 225; Indels 162; Gaps 22;

Qy [illegible] NMLSHHIAHRLF[illegible]NVTNV[illegible]TINHT[illegible]NYVKKFLDPNNYGANYIHIALQQVSMFTRS 142
Db 1 NFIMHEV[illegible]NMS[illegible]PA- --N[illegible]RYSKINIV[illegible]FCAYFVVYFA 34

Qy 143 [illegible] 212
Db 35 [illegible]KFEAINENFIINVKVIT[illegible]KF- ---------KPLCHE-----------IDILK 87

Qy 213 [illegible] 267
Db 88 SVKHPN[illegible]FTVP[illegible]FYIFFLI[illegible] 133

Qy 268 [illegible]IHASNVMLDCDTCRL------IDLEN 309
Db 134 N[illegible]IN INH N ASCHIEL[illegible]ALMENGEK 19[illegible]

Qy 310 [illegible]SLLGLPSFYRSYE[illegible]NLLPSVDVHC[illegible]YEMIYGRPP------------------ 351
Db 191 YIVI[illegible]FFFMA[illegible]MYEFQ[illegible]YN--EKVD[illegible]YAFGMCLLEMAIGEYPY[illegible]ENAVQVFKKVTQ 248

Qy 352 -----------------[illegible]LSVRVDSPPPAPSMAVVAVLPSTLSQPACKNIM[illegible]ISPRLIQMPL 395
Db 249 [illegible]IRPP[illegible]SRVL[illegible]PFLIIIVNI[illegible]PPDPRMTAQP[illegible]FRFL[illegible]AVEFEVVLVSRDMIMKL 306

Qy 396 FSDVLLLISEK[illegible]QEKIPIKLEEALKIAKECIEKRLIEEQKQ----IHQHRRLTAQS 449
Db 307 LIIQVVFKGMDK[illegible]VKFEFNADIPTAADVVASMIEEQVLQNCYQQLIT[illegible]INRILKEIAR 366

Qy 450 HHHSEFPPKKKKLIAPKKSKHSALENS------------------HHHS----ARY 482
Db 367 NQ[illegible]PK[illegible]VKPENT[illegible]PAFFF[illegible]ALAVEFVTPADE[illegible]HNIAEEKC 42[illegible]

Qy 483 SNSNNS[illegible]SPPPPPPPAAP--------LPPASI 532
Db 427 KE[illegible]AI[illegible]AKP[illegible] ----[illegible]QPQQPQPQPQPQPQQQIQLQYLSPQST 478

Qy 533 EVPAQLS SQAVNGMS[illegible]NPLKGHLRKAKIPDHSA 573
Db 479 LSP[illegible]ISLQNSINSIM[illegible]VSGDEQVEITTHSA 520

RESULT 9
[illegible]
serine/threonine protein kinase PpkA PA0074 [imported] - Pseudomonas aeruginosa (strain
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2002
C;Accession: [illegible]
R;Stover, C.K.; Pham, X.[illegible]; Erwin, A.L.; [illegible]; Westbrock-Wadman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, [illegible]; Lory, S.; Olson, M.V.
Nature [illegible]
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A;Reference number: A82[illegible]; MUID:20437337
A;Accession: [illegible]
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1032 <STO>
A;Cross-references: GB:AE004446; GB:AE004091; NID:g9945886; PIDN:AAG03464.1; GSPDB:GN001
A;Experimental source: strain PAO1
C;Genetics:
A;Gene: ppkA; PA0074

Query Match [illegible]; Score [illegible]; DB 2; Length 1032;
Best Local Similarity 21.7%; Pred. No. [illegible];
Matches 78; Conservative 47; Mismatches 1[illegible]; Indels 129; Gaps 1[illegible];

Qy 232 GTLKELIYKAKPE[illegible]IKKY[illegible]FPYGHLHA 291
Db 91 GTLKERIQ- - Q[illegible]AYV[illegible]QVAAALDYAHSQGIVHRDVKP 132

Qy 292 SNVMLDCDTCKLL DLENS [illegible]FKINILESVDVH 336
Db 133 ANILLKADGTAVL[illegible]LFGIAK[illegible]SRALLY 190

Qy 337 [illegible]HLLYEMIY[illegible]SVPVL[illegible]MAVVAVL[illegible]MPLISKLL 391
Db 191 ALGVVL[illegible] [illegible]KLESTALAHLIF 221

Qy 392 ---QMPL----FSDVLLLISEK PQEK[illegible]KIKEAL[illegible]KQIHQH 440
Db 222 [illegible]SAIFAIQI- - - - 272

Qy 441 [illegible]NSSPLISPS 506
Db 273 - RPLATPQ[illegible]PPA [illegible]PAFFAPLLPA[illegible]GG[illegible]PVSLQL 310

Qy 507 [illegible]PPSLSQLALPPPH [illegible]ALISS 554
Db 311 PPVIPSAGG--AIPPPPPPS[illegible]AAKPPS[illegible]AKLEA GGSKTPLIAA 358

RESULT 10
T34021
protein kinase SK2 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C;Accession: T34021
R;Fukami, Y.; Yamamoto, H.; Ichihara, T.; Mori, K.; [illegible], T.; Sato, K.
submitted to the EMBL Data Library, April 1997
A;Description: SK2, a putative rat homologue of yeast protein kinase NRK1.
A;Reference number: Z21463
A;Accession: T34021
A;Status: preliminary, translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1206 <FUK>
A;Cross-references: EMBL:AB003357; NID:[illegible]; PID:[illegible]; PIDN:BAA20077.1
A;Experimental source: strain SD
C;Genetics:
A;Gene: SK2

Query Match 5.3%; Score 1·8; DB 2; Length 1206;
Best Local Similarity 22.9%; Pred. No. 0.3·;
Matches 110; Conservative 58; Mismatches 19·; Indels 122; Gaps 1·;

Qy 11· LLVKKFLDPNNYGANYIHIALQQVSMFTRS[illegible]FPYKPNQE 172
Db 22 LEVKKFLNPRPP [illegible]KA N 5·

Qy 17· KLELVLSWAL[illegible]SMPSR 231
Db 54 KLLNVLAAAKV[illegible]LFSEFLLEPYMVC[illegible]APTYLNNAWILIEFCAG 113

Qy 232 GTLKDLIYKAK[illegible]KKY[illegible]VKFLHRKGFFYGHLHA 291
Db 114 GAVDAVMLELE--------- KPLIESQIQVV[illegible]KQILQALNYLHDNKIIHRDLKA 158

Qy 292 SNVM LDCD[illegible]KLLLENSLLS[illegible]YSCYF[illegible]EK 326
Db 159 GNILFTLDGDIKLADFGVSAKNTRT[illegible]YWMAPEVVMCETSKEEPYDYK 215

Qy 327 INILESVDVHCFGHLLYEMIYGRPP[illegible]VV[illegible]PPA PSMAVVAVLPSL 374

```
Db        216           ADVWSLGITLIEMALIEPPHHELNPMRVLLKIAKSEPPTLAQPSRWSSNFKDFL 269

Qy        375 LS  EA KN MR  SR   QMR  SDVLL   EKP  K      K       EALE AK   LKR 429

Db        270 KKCLEKNVDARWTTSQLLQHPF       VTVDSNKPVRELIAEAKAEVTEEVEDGKEEDEEE 325

Qy        430 LEEQKQTHQHRRLTEAQSHPGSEEKKEEKKELLAKKKSEKRSALENSEEHSARYSNSNNSG 489

Db        326 EEENSLPIPTNKRASSDLSIASSEEDK       LSQNACILESVSEKTEHS        NSE 373

Qy        490 SSASSSPISSPSSPIPPSSTSGTSALPPPPPPPPPPAAPLPPASTEVPAQLSSQAVNGMSRG 549

Db        374 EKEENKVLSTEKEGPES          PEKIVDVDGEANDVNLETVAEPNLQAVGPHENG 422


RESULT 11
[illegible]
serine/threonine protein kinase - guinea pig
N;Alternate names: STE20-like kinase
C;Species: Cavia porcellus (guinea pig)
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jul-2000
C;Accession: [illegible]
R;[illegible], Kuroda, Y.; Yamada, H.; Tsujikawa, K.; Mimura, T.; [illegible], Y.
Arch. Biochem. Biophys. 34[illegible], 201-207, 1997
A;Title: Molecular cloning and characterization of a novel protein kinase STE20-like kinase [illegible]
A;Reference number: [illegible]; MUID:97288344
A;Accession: [illegible]
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1231 <[illegible]>
A;Cross-references: EMBL:[illegible]; NID:g2911114; PIDN:BAA2493[illegible].1; PID:g2911114
A;Experimental source: strain Hartley; liver

  Query Match             5.3%;  Score 158;  DB 2;  Length 1231;
  Best Local Similarity   23.0%;  Pred. No. 0.37;
  Matches  1[illegible];  Conservative   58;  Mismatches  173;  Indels  134;  Gaps   19;

Qy        113 ELVKKEFLLFNNYGANYTETIALQQVIMEFKGLEKWEVVLLIKLIGWKIKKKYLIMEIENQF 172

Db         22 EHVKRDLNPEEF                          WEIIGELGD   GAFGKVY        KAQN 53

Qy        173 EKKIVLSWALSQLKYLSTEKIPQTKRLLESVGHTYYRVLIFATANKGALLIKMENLK 231

Db         74 EKENVLAAAKVIDTKSEEELEDYMVEIDILASCDHPNIVKLLDAFYYENNLWILIEFCAG 113

Qy        232 GILKGLYKAKEKSPELKKYTNPKKIQGLELQQIKTYGRQILEVLKFLHDKGFPYGHLHA 291

Db        114 GAVDAVMLELE                    RPLTESQIQVVCKQTLEALNYLHDNKIIHRDLKA 158

Qy        292 SNVM  LDGD                   TCRLLDLENSLSGLP                  GFYRGYFSQFRK 326

Db        159 GNILFTLDGDIKLADFGVSAKNTRTIQRRDSFIGTPYWMAPEVVMCETSKDRPYDYK      215

Qy        327 INTLESVDVHCFGHLLYEMTYGRPP   DSVPV           DSFPPA    FSMAVVAVLESI 374

Db        216           ADVWSLGITLIEMAEIEPPHHELNPMRVLLKIAKSEPPTLAQPSRWSSNFKDFL 269

Qy        375 LS  EA KN MR  SR   QMR  SDVLL   EKP  K  E  KELK       SALE AKE  LKR 429

Db        270 KKCLEKNVDARWTTSQLLQHPF       VTVDSNKPIRELIAEAKAEVTEEVEDGKEEDEEE 325

Qy        430 LEEQKQTHQHRRLTEAQSHPGSEEKKEEKKELLAKKKSEKRSALENSEEHSARYSNSNNSG 489

Db        326 EEENSLPIPTNKRASSDLSIASSEEDK       LSQNACILESVSEKTEHS         NSE 373

Qy        490 SSASSSPISSPSSPIPPSSTSGTSALPPPPPPPPPPA           APLPPASTEVP 535

Db        374 EKEGTKVLNEK                    DPSGEENAVELVGGAVAVLPDPATELP 412


RESULT 12
[illegible]
```

```
serine/threonine protein kinase - mouse
C;Species: Mus musculus (house mouse)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Accession: T14157
R;Pytowski, B.; Hicklin, D.J.; Kornhaber, G.; Bellaratta, D.V.; Witte, L.
submitted to the EMBL Data Library, December 1997
A;Reference number: Z17894
A;Accession: T14157
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1233 <PYT>
A;Cross-references: EMBL:AF039574; NID:g2773155; PID:g2773156; PIDN:AAB96682.1

  Query Match             5.2%;  Score 155.5;  DB 2;  Length 1233;
  Best Local Similarity   23.6%;  Pred. No. 0.51;
  Matches   98;  Conservative   56;  Mismatches  159;  Indels  103;  Gaps   17;

Qy        113 ELVKKEFLLFNNYGANYTETIALQQVIMEFKGLEKWEVVLLIKLIGWKIKKKYLIMEIENQF 172

Db         22 EHVKRDLNPEEF-----------------------WEIIGELGD   GAFGKVY        KAQN 53

Qy        173 EKKIVLSWALSQLKYLSTEKIPQTKRLLESVGHTYYRVLIFATANKGALLIKMENLK 231

Db         74 EKENVLAAAKVIDTKSEEELEDYMVEIDILASCDHPNIVKLLDAFYYENNLWILIEFCAG 113

Qy        232 GILKGLYKAKEKSPELKKYTNPKKIQGLELQQIKTYGRQILEVLKFLHDKGFPYGHLHA 291

Db        114 GAVDAVMLELE                    RPLTESQIQVVCKQTLEALNYLHDNKIIHRDLKA 158

Qy        292 SNVM  LDGD                   TCRLLDLENSLSGLP                  GFYRGYFSQFRK 326

Db        159 GNILFTLDGDIKLADFGVSAKNTRTIQRRDSFIGTPYWMAPEVVMCETSKDRPYDYK      215

Qy        327 INTLESVDVHCFGHLLYEMTYGRPP   DSVPV           DSFPPA    FSMAVVAVLESI 374

Db        216           ADVWSLGITLIEMAEIEPPHHELNPMRVLLKIAKSEPPTLAQPSRWSSNFKDFL 269

Qy        375 LS  EA KN MR  SR   QMR  SDVLL   EKP  K           EALE AK   LKR 429

Db        270 KKCLEKNVDASWTTSQLLQHPF       VTVDSNKPVRELIAEAKAEVTEEVEDGKEEDEEE 325

Qy        430 LEEQKQTHQHRRLTEAQSHPGSEEKKEEKKELLAKKKSEKRSALENSEEHSARYSNSN 484

Db        326 EALNAEPIPANRRASSDLSIASSEEDKLSQNACILESVSEKTEHS        NSEN 378


RESULT 13
E96636
hypothetical protein T7P1.21 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: E96636
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,
 .A.; Li, J.H.; Li, J.; Lin, X.; Liu, S.X.; Liu, A.; [illegible], [illegible]; Matti, [illegible]; Marzia
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719
A;Accession: E96636
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-907 <S10>
A;Cross-references: GB:AE005172; NID:g6751696; PIDN:AAF27[illegible].1; GSPDB:GN00141
C;Genetics:
A;Gene: T7P1.21
A;Map position: 1
```

```
Query Match 5.1%; Score 154.5; DB 2; Length 907;
Best Local Similarity 19.5%; Pred. No. 3.39;
Matches [illegible]; Conservative [illegible]; Mismatches [illegible]; Indels [illegible]; Gaps 22;

Qy   [illegible]
Db   [illegible] DLSIDDSPS[illegible] [illegible] 159

Qy   117 [illegible] WEKKKKLMKI 168
Db   [illegible] ANVEFY [illegible] 198

Qy   169 [illegible] SALLIFMP 228
Db   [illegible] LIEMS 221

Qy   229 [illegible]
Db   222 KPPPEMMIIDPPPPKK [illegible]

Qy   [illegible]
Db   [illegible] SKNSP[illegible] PIDVKRLA 425

Qy   340 [illegible]
Db   [illegible] VISVVE [illegible] 451

Qy   [illegible] 458
Db   [illegible] 388

Qy   [illegible] 493
Db   [illegible] 410

Qy   5[illegible] SSPTPPSISTISAIPP[illegible]PPPLPAA --------PLPPA 530
Db   441 [illegible]PIA TAISM[illegible]PPLAVMELKHFAPPPPPPLPPA 483
```

RESULT 14
KIRICE
protein kinase C (EC 2.7.1.-) epsilon - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 11-Jun-1999
C;Accession: B28[illegible]; B29406; S0[illegible]216
R;Ono, Y.; Fujii, T.; [illegible]; Kikkawa, U.; Igarashi, K.; Nishizuka, Y.
J. Biol. Chem. 263, 6927-6932, 1988
A;Title: The structure, expression, and properties of additional members of the protein
A;Reference number: A92717; MUID:88198270
A;Accession: B28[illegible]
A;Molecule type: DNA
A;Residues: 1-737 <ON>
A;Cross-references: GB:M18331; NID:g206182; PIDN:AAA41872.1; PID:g206183
R;Housey, G.M.; O'Brian, C.A.; Johnson, M.D.; Kirschmeier, P.; Weinstein, I.B.
Proc. Natl. Acad. Sci. U.S.A. 84, 1065-1069, 1987
A;Title: Isolation of cDNA clones encoding protein kinase C: evidence for a protein kina
A;Reference number: A94145; MUID:87147[illegible]
A;Accession: B294[illegible]
A;Molecule type: mRNA
A;Residues: [illegible]-[illegible],'[illegible]',467,'LSNPFLLLLPDQ[illegible]PPLLRQ',487-545,'C',547-636
A;Cross-references: GB:M155[illegible]; NID:g206192; PIDN:AAA41877.1; PID:g206193
C;Comment: Protein kinase C eps[illegible] and epsilon' appear to be encoded by the same gene
C;Function:
A;Description: catalyzes [illegible] phosphate [illegible]
A;Note: activity is calcium-independent, phospholipid-dependent, and activated by diacyl
C;Superfamily: protein kinase C delta; protein kinase C zinc-binding repeat homology; pr
C;Keywords: alternative splicing; ATP; autophosphorylation; duplication; phorbol ester b
F;15[illegible]-1[illegible]/Region: pseudophosphorylation motif
F;170-220/Domain: protein kinase C zinc-binding repeat homology <KZ1>
F;243-292/Domain: protein kinase C zinc-binding repeat homology <KZ2>
F;406-668/Domain: protein kinase homology <KIN>
F;414-422/Region: protein kinase ATP-binding motif
F;17[illegible],201,204,220/Binding site: zinc (His, Cys, Cys, Cys) #status predicted
F;183,186,209,212/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
F;24[illegible],273,27[illegible],292/Binding site: zinc (His, Cys, Cys, Cys) #status predicted
F;256,259,281,284/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
F;437,45[illegible],5[illegible]2,5[illegible]4/Active site: Lys, [illegible], Asp, Lys #status predicted
F;703,710/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status p

```
Query Match 5.1%; [illegible]; Length [illegible];
Best Local Similarity 22.9%; Pred. No. 0.34;
Matches 75; Conservative 47; Mismatches 12[illegible]; Indels 79; Gaps 1[illegible];

Qy   162 KYFLMKIKNQPKERLVLSWADLGP[illegible]KYLSDE[illegible] LLPSCLPFYIYRVTFAIA 217
Db   4[illegible] [illegible]VMLAL[illegible] VYAVEV[illegible] [illegible]LIQLYC[illegible]FQ 477

Qy   21[illegible] [illegible] 277
Db   478 TKERLFFVMEYVNG[illegible] LMFQI[illegible]KS [illegible] [illegible]YAAEVTIALM 521

Qy   278 FLHDKGPPYCHLHASNVMLD[illegible] T[illegible] [illegible]NSLLDGLPSFY[illegible]SYF[illegible]QF 324
Db   522 [illegible] 580

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Db   581 [illegible]LLYG[illegible]VEWWALGVLMYEMMAG[illegible]AENE[illegible]VLYPVWLS[illegible]AVS[illegible]K 639

Qy   373 S TLSCHACKNGMPTISPLLQMPLE[illegible] V[illegible]K[illegible]PKI[illegible]KLKE 417
Db   640 A[illegible] [illegible]VAA[illegible] [illegible]KR[illegible]VN 696

Qy   418 ALSIAEP[illegible]IPKRLIEEQ 434
Db   697 NFDQDFTREEPILTLVDEAIVKQINQEE 724
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RESULT 15
T15264
hypothetical protein F59E12.9 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Accession: T15264
R;Johnson, D.
submitted to the EMBL Data Library, May 1997
A;Description: The sequence of C. elegans cosmid F59E12.
A;Reference number: Z18318
A;Accession: T15264
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1621 <JOH>
A;Cross-references: EMBL:AF003386; NID:g[illegible]; PIDN:AAB542[illegible]
A;Experimental source: strain Bristol N2; clone F59E12
C;Genetics:
A;Gene: CESP:F59E12.9
A;Map position: 2
[illegible]

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Query Match 5.1%; Score 15[illegible]; DB 2; Length 1621;
Best Local Similarity 19.5%; Pred. No. 0.4[illegible];
Matches 114; Conservative 79; Mismatches [illegible]; Indels [illegible]; Gaps 29;

Qy   1[illegible] NV[illegible]LVFFFLLIN [illegible]FDI 155
Db   868 NIGTT ENFPMLIVVLRPNFAERF[illegible] [illegible] 9[illegible]
Qy   156 GWFIKKKYFLMKIKNQPKERLVLSW AE[illegible] [illegible]SCLHP 20[illegible]
Db   917 [illegible] ENEEKE [illegible]NISEAVNESTES 962
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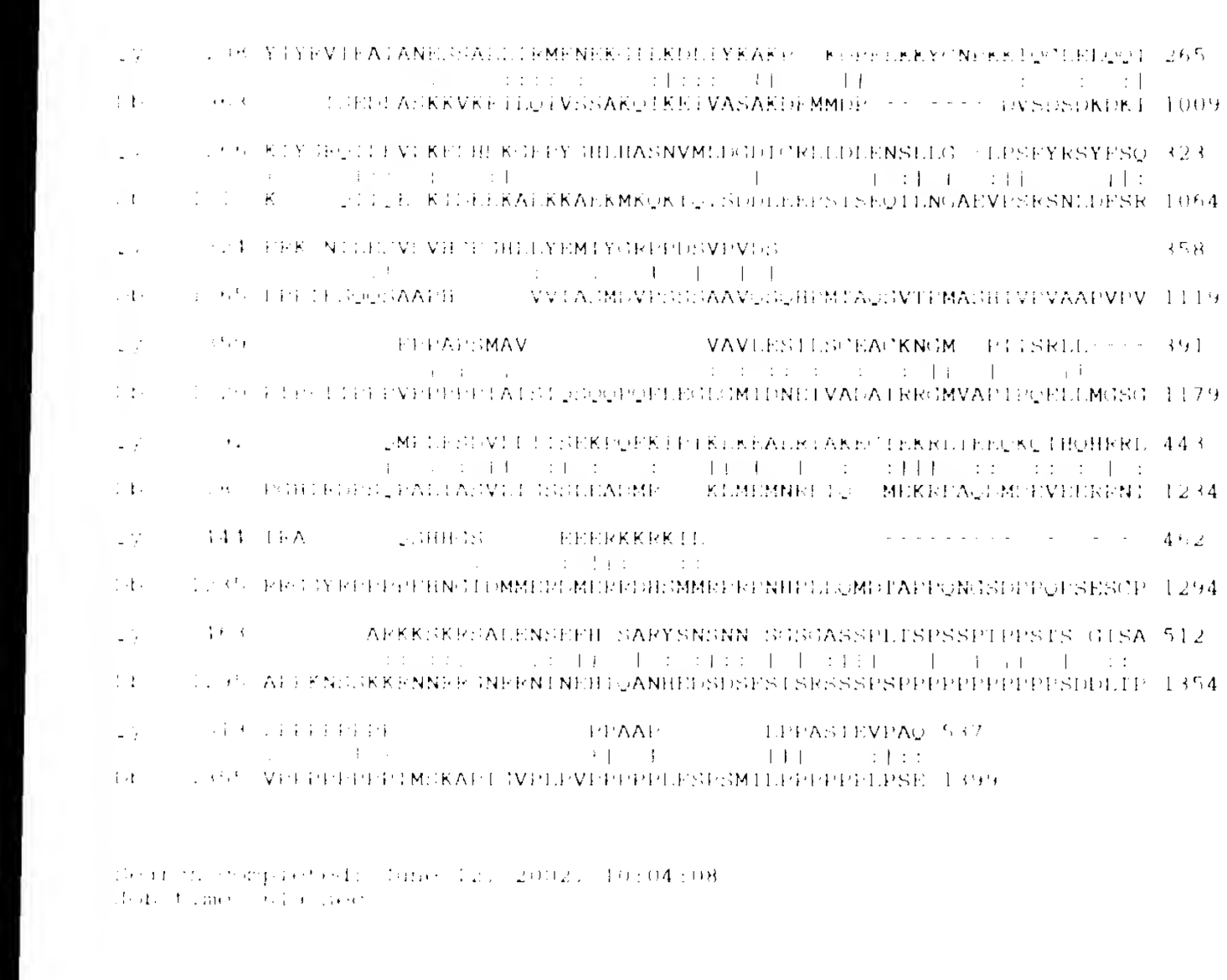

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Db   [illegible]     LEEEASKKVKEILQIVSSAKQIKEIVASAKDEMMDP ---------DVSDSDKDKI 1009

Qy   [illegible] KIY DEQIIEVIKEIHEKGEEY HHIIASNVMIDGDIGRIEIDLENSLLG  LPSEYKSYESQ 323
Db   [illegible] K     QIIIE KIEEEKAIKKAEKMKQKIQ SDDIEEESISEQIINGAEVESRSNLDESR 1064

Qy   [illegible] EEK NIIEIVEVIEIDHELYEMIYGRPPDSVPVDS                        358
Db   [illegible] EPEIEGQQSAAPH       VVIAQMDVPSSSAAVQSQHPMIAQSVTPMASHIVPVAAPVPV 1119

Qy   [illegible]           EEPAPSMAV               VAVIESIISCEACKNGM   PIISRLL---- 391
Db   [illegible] EEPEIEEEVPPPPPIAISIQQQQPQPLEGISMIDNEIVADAIRRGMVAPIPQELLMGSG 1179

Qy   [illegible]           QMEIESDVIEIISEKPQPKIPIKEKEALKIAKKQIEKRLIEEQKQIHQHERL 443
Db   [illegible] PDIEDESQPALIASVLIDSSLEADMP   KLMEMNKEIQ  MEKRPAQLMEEVEIERENI 1234

Qy   [illegible] IEA       QSHHES      EEERKKRKIL             ---------- -  ---- 462
Db   [illegible] PEGDYPEEEPPERNGIDMMEPDMEPPDHSMMEPRPNHPLLQMDTAPPQNGSDPPQPSESCP 1294

Qy   [illegible]          AEKKSKRSALENSEEH SARYSNSNN SGSGASSPLISPSSPIPPSIS GISA 512
Db   [illegible] AEEKNSSKKENNEKGNEKNINEHIQANHEDSDSESISRSSSPSPPPPPPPPPPPSDDLIP 1354

Qy   [illegible] [illegible]                  PPAAP         LPPASIEVPAQ 537
Db   [illegible] VEEPEEEEPIMSKAPLIVPLPVEPPPPLESPSMILPPPPPELPSE 1399
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Search completed: June 12, 2002, 10:04:08
Job time: [illegible] secs

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

M protein - protein search, using sw model

Run on: June 12, 2002, 09:54:44 ; Search time 106.75 Seconds
(without alignments)
600.871 Million cell updates/sec

Title: US-09-684-458-2
Perfect score: 8001
Sequence: 1 MAFMEEGAGEEIIMEVEL ..... EQKCILRDAETRHSAREC 577

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 211079796 residues

Total number of hits satisfying chosen parameters. 747574

Minimum DB seq length:
Maximum DB seq length: 2000000000

Post-processing: Minimum Match: 0%
Maximum Match: 100%
Listing first 45 summaries

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7: /cgn2_6/ptodata/2/aa/A_Geneseq_082802.pep:* ; pub|AA1986 DAT *
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22: /cgn2_6/ptodata/2/aa/A_Geneseq_082802.pep:* ; pub|AA2001 DAT *

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	8001	100.0	577	22	AAF02775	Human PRK2 C-MG.2 p
2	1461.5	18.3	949	22	AAB65080	Novel protein kina
3	874	10.9	663	22	ABB59405	Drosophila melanog
4	826	10.3	155	21	AAB32078	Human secreted pro
5	535	6.7	141	22	AAU17470	Novel signal trans
6	492.5	6.2	515	22	ABB62663	Drosophila melanog
7	492.5	6.2	515	22	ABB62672	Drosophila melanog
8	332	4.2	157	21	AAB32077	Human secreted pro
9	233.5	2.9	496	22	AAM38834	Human polypeptide
10	231.5	2.9	496	22	AAM40620	Human polypeptide
11	206.5	2.6	146	20	AAW87772	Human serum gluco
12	199.5	2.5	912	20	AAY59934	Human GPK2 protein
13	199.5	2.5	968	20	AAY59966	Full length human
14	195	2.4	1081	21	AAY64969	Amino acid sequence
15	180.5	2.3	911	20	AAY59957	Mouse STE20-relate
16	172.5	2.2	446	22	AAB95616	Novel protein kina
17	172.5	2.2	1533	22	AAB20179	Novel human diagno
18	172	2.2	1513	22	AAB35581	Human protein kina
19	171.5	2.1	502	22	AAM38236	Human polypeptide
20	164.5	2.1	1043	22	ABB71412	Drosophila melanog
21	162.5	2.0	407	22	ABB24350	Drosophila melanog
22	162	2.0	873	22	AAM38436	Human protein SEQ
23	161	2.0	541	19	AAW57148	Mammalian Eka (Mou
24	160.5	2.0	754	22	AAB65512	Human protein sequ
25	158.5	2.0	591	22	AAM38437	Human polypeptide
26	157.5	2.0	661	22	AAL37846	Human protein kina
27	157.5	2.0	661	22	AAL37847	Human protein kina
28	157.5	2.0	1189	22	ABB59904	Drosophila melanog
29	157.5	2.0	1920	22	AAB95659	Novel protein kina
30	156	2.0	429	21	AAY05278	Human serum and gl
31	155.5	1.9	227	22	AAM39972	Human polypeptide
32	155.5	1.9	464	22	AAM38734	Human polypeptide
33	155.5	1.9	1069	22	AAB95508	Human protein kina
34	155.5	1.9	1202	21	AAB85521	A marine Ste20-rel
35	154.5	1.9	894	22	AAM38435	Human protein SEQ
36	154.5	1.9	1297	16	AAK84648	mSOS2 protein. Mu
37	153	1.9	1504	22	AAB65734	Human protein sequ
38	152.5	1.9	1068	22	AAM74228	Human protein SEQ
39	152.5	1.9	1078	22	AAM38437	Human polypeptide
40	152.5	1.9	1089	22	ABG20963	Novel human diagno
41	152.5	1.9	1297	14	AAR47148	Mammalian son of s
42	152	1.9	429	21	AAB12313	Human serine thron
43	152	1.9	951	22	AAB15834	Human polypeptide
44	151.5	1.9	212	22	AAU12902	Novel signal trans
45	151.5	1.9	841	22	AAB95648	Human KIAA protein

ALIGNMENTS

RESULT 1
AAF02775
ID AAF02775 standard; protein; 577 AA.
XX
AC AAF02775;
XX
DT 06-AUG-2001 (first entry)
XX
DE Human PRK2 C-MG.2 protein sequence, SEQ ID NO:2.
XX
KW Human; gene therapy; proliferative vascular disease; restenosis; cardiac hypertrophy;
KW congestive heart failure; CHF; myocardial infarction; aortic stenosis;
KW [illegible]; vaccine; endothelial disease; DNA-C-MG.2 1776 cDNA; PRO-C-MG.2 protein.
XX
OS Homo sapiens.
XX

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FT	Modified-site	54..58
FT		/note= "cAMP- and cGMP-dependent protein kinase phosphorylation site"
FT	Modified-site	57..61
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FT	Modified site	110..114
FT		/note= "Casein kinase II phosphorylation site"
FT	Modified-site	116..125
FT		/note= "Tyrosine kinase phosphorylation site"
FT	Modified site	179..183
FT		/note= "Casein kinase II phosphorylation site"
FT	Modified-site	190..194

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PN   W[illegible]-A2.
XX
PD   [illegible]-APR-2001.
XX
PF   [illegible]-OCT-2000; 2000WO-US27512.
XX
PR   07-OCT-1999;   99US-0158587.
PR   [illegible]-OCT-1999;   99US-0162611.
XX
PA   (GETH ) GENENTECH INC.
PA   (CURA ) CURAGEN CORP.
XX
PI   Gerritsen ME,  Goddard A,  Grimaldi JC,  Mehraban F;
XX
DR   WPI; 2001-[illegible]/[illegible].
DR   N-PSDB; AA[illegible].
XX
PT   Polypeptides critical for angiogenesis and vascularization, and the
PT   nucleic acids encoding them, useful for treating conditions related to
PT   inappropriate vascularization and angiogenesis
XX
PS   Claim 1; Page 154-155; 180pp; English.
XX
CC   The patent discloses novel polypeptides critical for angiogenesis and
CC   vascularisation and nucleic acids encoding them. The sequences of the
CC   present invention are used in the prevention, treatment and diagnosis
CC   of diseases associated with inappropriate angiogenesis and/or neo- or
CC   cardiovascularisation. They are used in the diagnosis, prevention
CC   or treatment of angiogenic disorders such as cardiac hypertrophy,
CC   congestive heart failure (CHF), myocardial infarction, aortic stenosis,
CC   arterial restenosis and vascular trauma such as wounds, burns or
CC   surgery. They are also used in the treatment of cancer and endothelial
CC   diseases. The proteins of the invention are used as antigens in the
CC   production of antibodies against the angiogenesis and vascularisation
CC   proteins and in assays to identify modulators (agonists and antagonists)
CC   of their expression and activity. The antibodies and antagonists are
CC   used to down regulate expression and activity of the protein of the
CC   invention. The antibodies are also used as diagnostic agents for
CC   detecting the presence of the proteins of the invention in samples.
CC   The sequences of the invention are also used as vaccines and in gene
CC   therapy. The present sequence is novel human PRO-C MCL2 protein
CC   which is encoded by DNA C MCL2 1776 cDNA clone of the invention.
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SQ   Sequence  577 AA;

  Query Match             100.0%;  Score 3001;  DB 22;  Length 577;
  Best Local Similarity   100.0%;  Pred. No. 4.5e-229;
  Matches  577;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MATMEKPPAQKVLIDDTVPLTAAIEASQSLQSHTEYIIRVQRQISVENSWQIVRRYSDFD 60
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Qy         61 LLNNSLQIAGLSLPLPPKKLIGNMDREFIAERQKGLQNYLNVITTNHILSNCELVKKFLD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 llnnslqiaglslplppkkligmdrefiaerqkglqnylnvittnhilsncelvkkfld 120

Qy        121 PNNYSANYTEIALQQVSMFFRSEPKWEVVEPLKDIGWRIRKKYFLMKIKNQPKERLVLSW 180
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Db        121 pnnysanyteialqqvsmffrsepkwevveplkdigwrirkkyflmkiknqpkerlvlsw 180

Qy        181 ADLGPDKYLSDKDFQCLIKLLPSCLHPYIYRVTFATANESSALLIRMFNEKGTLKDLIYK 240
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Db        181 adlgpdkylsdkdfqclikllpsclhpyiyrvtfatanessallirmfnekgtlkdliyk 240

Qy        241 AKPKDPFLKKYCNPKKIQGLELQQIKTYGRQILEVLKFLHDKGFPYGHLHASNVMLDGDT 300
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Db        241 akpkdpflkkycnpkkiqglelqqiktygrqilevlkflhdkgfpyghlhasnvmldgdt 300

Qy        301 CRLLDLENSLLGLPSFYRSYFSQFRKINTLESVDVHCFGHLLYEMTYGRPPDSVPVDSFP 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 crlldlensllglpsfyrsyfsqfrkintlesvdvhcfghllyemtygrppdsvpvdsfp 360

Qy        361 PAPSMAVVAVLESTLSCEACKNGMPTISRLLQMPLFSDVLLTTSEKPQFKIPTKLKEALR 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 papsmavvavlestlsceackngmptisrllqmplfsdvllttsekpqfkiptklkealr 420

Qy        421 IAKECIEKRLIEEQKQIHQHRRLTRAQSHHGSEEERKRRKILARKKSKRSALENSEEHSA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 iakecieklrieeqkqihqhrrltraqshhgseeerkrrkilarkkskrsalenseehsa 480

Qy        481 RYSNSNNSGSGASSPLTSPSSPTPPSTSGISALPPPPPPPPPPAAPLPPASTEVPAQLSS 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        541 QAVNGMSRGALLSSIQNFQKGTLRKAKTCDHSAPKIG 577
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Db        541 qavngmsrgallssiqnfqkgtlrkaktcdhsapkig 577


RESULT 2
AAB65680
ID   AAB65680 standard; Protein; 649 AA.
XX
AC   AAB65680;
XX
DT   27-MAR-2001  (first entry)
XX
DE   Novel protein kinase, SEQ ID NO: 208.
XX
KW   Human, mouse, protein kinase, antiarthritic, antisclerotic; osteopathic;
KW   immunosuppressive; cardiant; renal; antiinflammatory; antiasthmatic;
KW   dermatological; antidiabetic; antiinfertility; gene therapy; vaccine;
KW   immune disorder; cardiovascular disease; neurodegenerative disease;
KW   cancer; autoimmune disorder; stroke; inflammatory bowel disease;
KW   inflammatory pelvic disease; multiple sclerosis; psoriasis.
XX
OS   Homo sapiens.
XX
PN   WO200073469-A2.
XX
PD   07-DEC-2000.
XX
PF   26-MAY-2000; 2000WO-US14842.
XX
PR   28-MAY-1999;   99US-0136503.
XX
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PA   (SUGE-) SUGEN INC.
XX
PI   Plowman GD, Martinez R, Whyte D, Sudarsanam S;
XX
DR   WPI; 2001-[illegible]/44.
DR   N-PSDB; AAF41[illegible]08.
XX
PT   Nucleic acids encoding kinase polypeptides, useful for diagnosing and
PT   treating immune-related diseases and disorders, cardiovascular disease,
PT   neurodegenerative diseases and/or cancers -
XX
PS   Claim [illegible]; [illegible]; [illegible]pp; English.
XX
CC   The present sequence is a novel protein kinase. The novel protein kinases
CC   and the nucleic acids that encode them may be used in the treatment and
CC   diagnosis of diseases associated with inappropriate kinase expression
CC   such as immune-related diseases and disorders, cardiovascular disease,
CC   neurodegenerative diseases and/or cancers. The nucleic acids and
CC   complementary sequences may also be used as DNA probes in diagnostic
CC   assays. The kinase polypeptides may be used as antigens in the production
CC   of antibodies of kinase expression and activity. Anti kinase antibodies
CC   and kinase antagonists may also be used to down regulate kinase
CC   expression and activity. Diseases related to kinase expression and
CC   activity include rheumatoid arthritis, atherosclerosis, autoimmune
CC   disorders, complications of organ transplantation, myocardial infarction,
CC   immune disorders, cardiomyopathies, strokes, renal failure,
CC   oxidative stress related disorders, chronic inflammatory bowel disease,
CC   chronic inflammatory pelvic disease, multiple sclerosis, asthma,
CC   osteoarthritis, psoriasis, rhinitis, autoimmunity, diabetes, cancers and
CC   reproductive disorders.
XX
SQ   Sequence [illegible] AA;

  Query Match             [illegible]7.3%;  Score 2919.5;  DB 22;  Length 649;
  Best Local Similarity   [illegible];  Pred. No. 1.5e-222;
  Matches  5[illegible];  Conservative    [illegible];  Mismatches    6;  Indels   13;  Gaps    2;

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Db          1 matmekppnakv[illegible]yiirvqqtisve[illegible]wqivrrysdfd 60

Qy         61 [illegible]LNNS[illegible]NMI[illegible]NVI[illegible]N[illegible]NCELVKKFLD 120
Db         61 [illegible]lnnsl[illegible]alsip[illegible]ppkk[illegible]qpylnvittnhilsnceelvkktld 120

Qy        121 FNPY[illegible]EWIVVL[illegible]W[illegible]LMK[illegible]KEELVLSW 180
Db        121 pnaysanyteial[illegible]pkw[illegible] 180

Qy        181 A[illegible]YTLEVILAIANESSAL[illegible]EMFN[illegible]LKDLIYK 240
Db        181 [illegible]k 240

Qy        241 AKPK[illegible]LKKY[illegible]N[illegible]YC[illegible]VLKFLH[illegible]PPY[illegible]HLHASNVMLDCDT 300
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Qy        361 PA[illegible]MAV[illegible]ELEKELAIR 420
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Qy        541 QQAVNQMSRGALLSSIQNPQKSTLKKAE[illegible]DSAPK[illegible] 57[illegible]
Db        541 qqavnqmsrgallssiqnpqk[illegible] 5[illegible]

RESULT 3
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ID   ABB59495 standard; Protein; 563 AA.
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AC   ABB59495;
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DT   26-MAR-2002  (first entry)
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DE   Drosophila melanogaster polypeptide SEQ ID NO 5277.
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KW   Drosophila; developmental biology; cell signalling; insecticide;
KW   pharmaceutical.
XX
OS   Drosophila melanogaster.
XX
PN   WO200171042-A2.
XX
PD   27-SEP-2001.
XX
PF   23-MAR-2001; 2001WO-US09231.
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PR   23-MAR-2000; 2000US-191637P.
PR   11-JUL-2000; 2000US-0614150.
XX
PA   (PEKE ) PE CORP NY.
XX
PI   Venter JC,  Adams M,  Li PWD,  Myers EW;
XX
DR   WPI; 2001-656860/75.
DR   N-PSDB; ABL03598.
XX
PT   New isolated nucleic acid detection reagent for detecting 1000 or more
PT   genes from Drosophila and for elucidating cell signalling and cell-cell
PT   interactions -
XX
PS   Disclosure; SEQ ID NO 5277; 21pp + Sequence Listing; English.
XX
CC   The invention relates to an isolated nucleic acid detection reagent
CC   capable of detecting 1000 or more genes from Drosophila. The invention is
CC   useful in developmental biology and in elucidating cell signalling and
CC   cell-cell interactions in higher eukaryotes for the development of
CC   insecticides, therapeutics and pharmaceutical drugs. The invention
CC   discloses genomic DNA sequences (ABL[illegible]), expressed DNA
CC   sequences (ABL01840 ABL16175) and the encoded proteins
CC   (ABB57[illegible]7 ABB72072).
CC   The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence   563 AA;

  Query Match             29.1%;  Score 874;  DB 22;  Length 563;
  Best Local Similarity   36.2%;  Pred. No. 1.2e-[illegible];
  Matches  295;  Conservative  [illegible];  Mismatches  [illegible];  Indels   84;  Gaps   11;

Qy         84 [illegible]CMEFRSE 143
Db          1 [illegible] 6[illegible]

Qy        144 EWLVVELLEDLWE[illegible]KYLMKIKNGPKES[illegible] 175
Db         6[illegible] [illegible] 1[illegible]

Qy        176 [illegible]LVLSWAE[illegible]YIYEVIFAIANELSA 222
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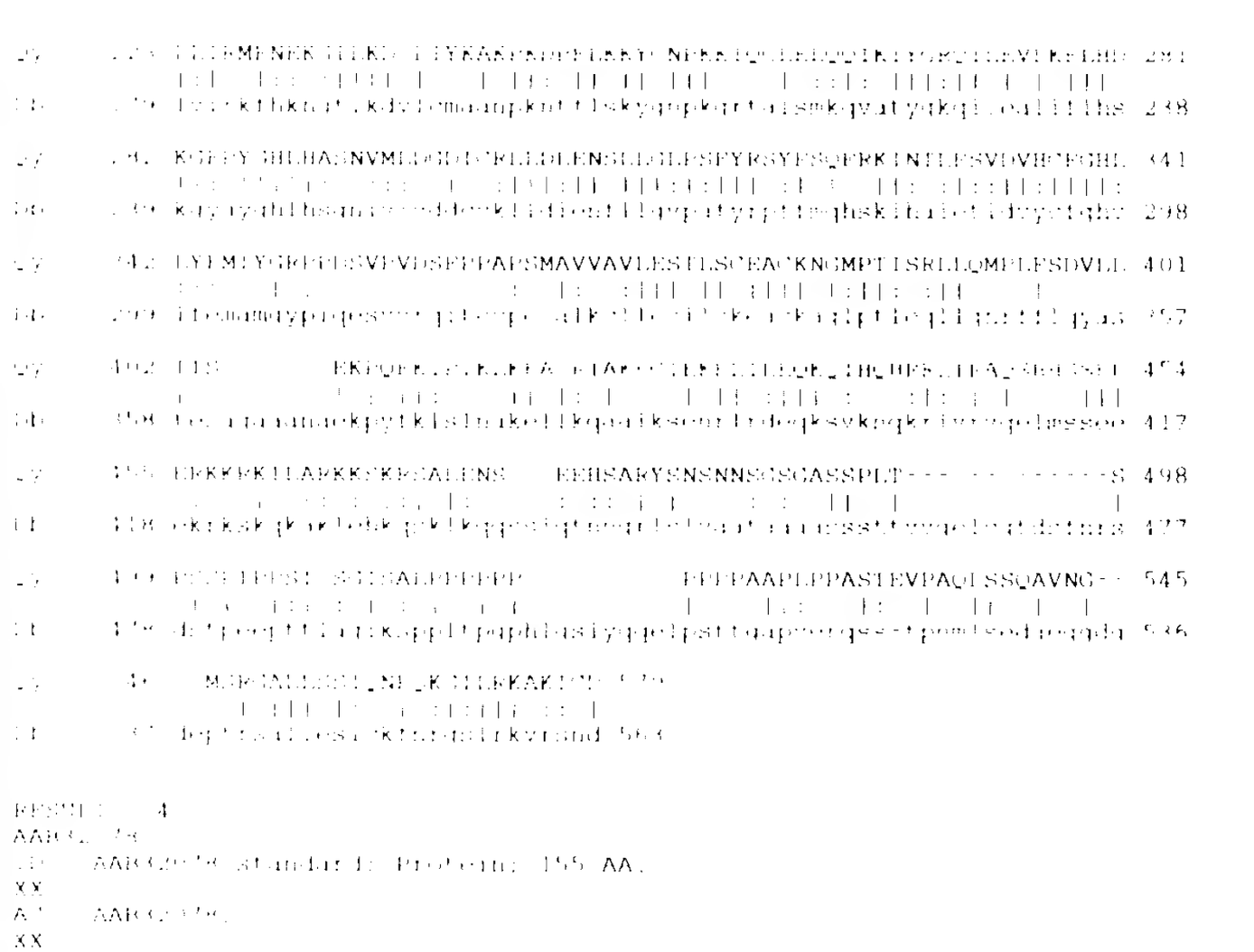
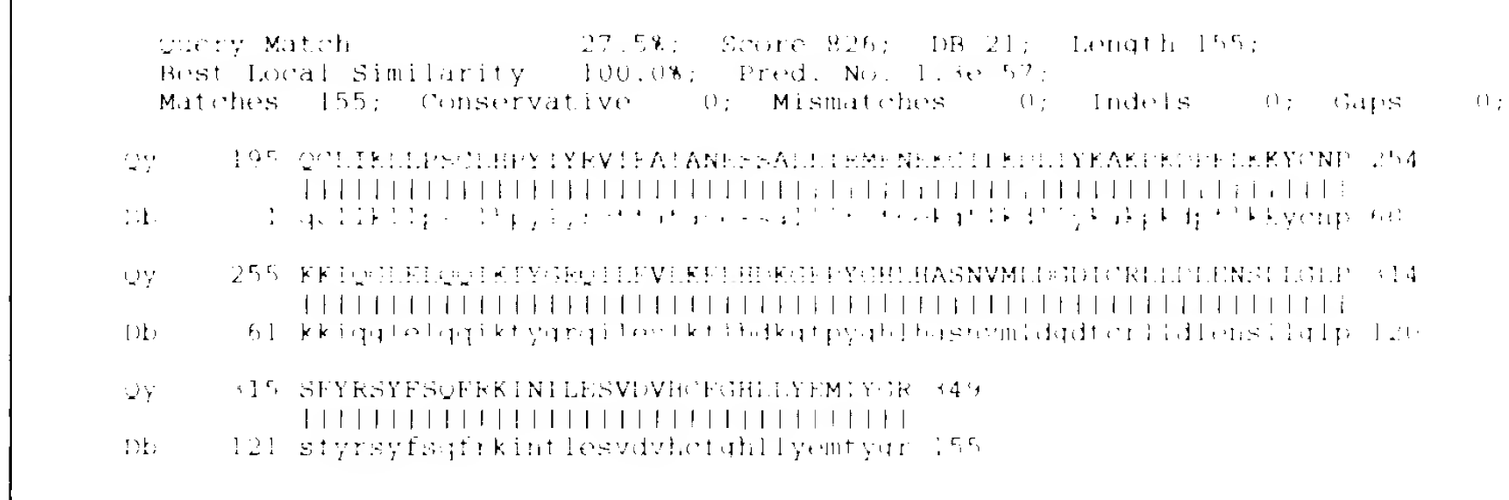


RESULT 4
AAB62002
ID AAB62002 standard; Protein; 155 AA.
XX
AC AAB62002;
XX
DT 14-FEB-2002 (first entry)
XX
DE Human secreted protein BCAST search protein SEQ ID NO: 136.
XX
KW cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
KW antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer;
KW antiherpetic; antioxidant; antibacterial; antifungal; antiparasitic;
KW cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
KW gastrointestinal disease; infection; human; secreted protein.
XX
OS Homo sapiens.
XX
PN WO200178483-A1.
XX
PD 26-OCT-2001.
XX
PF 22-MAR-2000; 2000WO-US07483.
XX
PR 20-MAR-1999; 99US-0125550.
PR 11-DEC-1999; 99US-0170562.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
IN Rosen CA; Ruben SM; Komatsoulis G;
XX
DR WPI; 2002-061257/07.
XX
PT Nucleic acid molecules encoding human secreted proteins, used in
PT preventing, treating or ameliorating a disorder, e.g. Alzheimer's and
PT Parkinson's diseases and cancers
XX
PS Sequence, Page 395-396; 423pp; English.
XX
CC The invention relates to the isolation of genes AAC66410-C66458 encoding
CC the human secreted proteins AAB62002-B62056. This sequence represents a
CC fragment of the protein encoded by the gene given in the descriptor
CC line. The sequence is used as a query sequence for doing BLASTX searches
CC to determine homologous sequence to the protein. The genes and proteins
CC are useful for preventing, ameliorating or treating medical conditions,
CC e.g. by protein or gene therapy. The genes are isolated from a range of
CC human tissues disclosed in the specification. The nucleic acids,
CC proteins, antibodies and (ant)agonists are useful in the diagnosis,
CC treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer,
CC and other cancers of the adrenal gland, bone, bone marrow, breast,
CC gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders
CC e.g. Addison's disease, allergies, autoimmune haemolytic anaemia,
CC autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple
CC sclerosis, rheumatoid arthritis and ulcerative colitis; (c)
CC cardiovascular disorders, such as myocardial infarction; (d) wound
CC healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and
CC (f) infectious diseases such as viral, bacterial, fungal and parasitic
CC infections.
XX
SQ Sequence 155 AA;



RESULT 5
AAU17470
ID AAU17470 standard; Protein; 141 AA.
XX
AC AAU17470;
XX
DT 07-NOV-2001 (first entry)
XX
DE Novel signal transduction pathway protein, Seq ID 1035.
XX
KW Neuroprotective; cytostatic; dermatological; immunosuppressive; tumour;
KW antiinflammatory; anti-HIV; antibacterial; antiinflammatory; cancer;
KW immune system disorder; rheumatoid arthritis; inflammatory condition;
KW organ transplant rejection; infection; hepatitis C; blood disorder;
KW sickle cell anaemia; hyperproliferative disorder; Gaucher's disease;
KW neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
KW chromosomal abnormality; Down syndrome; ischaemia; renal disorder;
KW cardiovascular; respiratory; wound healing; endocrine; Addison's disease;
KW reproductive system; gastrointestinal; liver disorder; AIDS;
KW acquired immune deficiency syndrome.
XX
OS Homo sapiens.
XX
PN WO200154733-A1.
XX
PD 02-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US01312.
XX
PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186850.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.

PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
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PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216883.
PR 11-JUL-2000; 2000US-0217487.
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PR 14-JUL-2000; 2000US-0218200.
PR 27-JUL-2000; 2000US-0220983.
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PR 14-AUG-2000; 2000US-0224518.
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PR 14-AUG-2000; 2000US-0224514.
PR 14-AUG-2000; 2000US-0224566.
PR 14-AUG-2000; 2000US-0224567.
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PR 18-AUG-2000; 2000US-0226274.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226868.
PR 22-AUG-2000; 2000US-0227182.
PR 28-AUG-2000; 2000US-0227829.
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PR 05-SEP-2000; 2000US-0229514.
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PR 06-SEP-2000; 2000US-0230427.
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PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
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PR 14-SEP-2000; 2000US-0232401.
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PR 21-SEP-2000; 2000US-0234225.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
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PR 26-SEP-2000; 2000US-0235484.
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PR 29-SEP-2000; 2000US-0236427.
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PR 02-OCT-2000; 2000US-0236802.
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PR 03-OCT-2000; 2000US-0238485.
PR 04-OCT-2000; 2000US-0239067.
PR 20-OCT-2000; 2000US-0240960.
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PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
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PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
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PR 08-NOV-2000; 2000US-0246542.
PR 08-NOV-2000; 2000US-0246609.
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PR 08-NOV-2000; 2000US-0246611.
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PR 17 NOV-2000; 2000US-0249211.
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PR 05-DEC-2000; 2000US-0251030.
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PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08 DEC 2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
DR WPI; 2001-465460/50.
DR N-PSDB; AAS27387.
XX
PT Novel polypeptides useful for diagnosing, treating, preventing and/or
PT prognosing disorders related to the proteins, including cancers, immune
PT disorders and neuronal disorders
XX
PS Claim 1; SEQ ID No 1035; 880pp; English.
XX
CC The invention relates to novel isolated polypeptides (I), and
CC polynucleotides (II). (I), (II) and the antibody to (I) are useful for
CC diagnosing, preventing and treating diseases including immune system
CC disorders (e.g. congenital and acquired immunodeficiencies, autoimmune

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CC   disorders (e.g. rheumatoid arthritis), inflammatory conditions, organ
CC   transplant rejection, graft versus host disease, infectious diseases
CC   (e.g. hepatitis C), bleeding disorders, haemoglobin abnormalities and
CC   other blood related disorders (sickle cell anaemia), myeloproliferative
CC   disorders, primary haematopoietic disorders, hyperproliferative
CC   disorders (e.g. Sezary's disease and cancer), neurodegenerative
CC   disorders (e.g. Alzheimer's disease, Parkinson's disease), chromosomal
CC   abnormalities (Down syndrome), ischaemic injury (e.g. stroke), renal
CC   disorders (e.g. glomerulonephritis), cardiovascular disorders
CC   (e.g. arrhythmia), respiratory disorders, dermatological disorders, in
CC   wound healing, epithelial cell proliferation, endocrine disorders (e.g.
CC   Addison's disease), reproductive system disorders, gastrointestinal
CC   disorders (inflammatory disorders), liver disorders (cirrhosis),
CC   disorders of B cell responsiveness to pathogens, activators of
CC   T cells, to induce higher affinity antibodies, and as a means to induce
CC   tumour tolerance in pathologies (e.g. acquired immune deficiency
CC   syndrome (AIDS)). AAB17655-AAB17683 represent novel signal transduction
CC   pathway proteins. Amino acid sequences of the invention.
XX

  Query Match          [illegible]; Score [illegible]; DB [illegible]; Length 141;
  Best Local Similarity  95.00%; Pred. No. 8.4e-38;
  Matches  133; Conservative  [illegible]; Mismatches  [illegible]; Indels  [illegible]; Gaps  [illegible];

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        [illegible]
Db      [illegible]

Qy      [illegible]
        [illegible]
Db      [illegible]

RESULT [illegible]
AAB17683 standard; protein; 515 AA.
XX
AC   AAB17683;
XX
DT   [illegible] (first entry)
XX
DE   Drosophila melanogaster polypeptide SEQ ID No 14781.
XX
KW   Drosophila; developmental biology; cell signalling; insecticide;
KW   pharmaceutical.
XX
OS   Drosophila melanogaster.
XX
PN   WO200171042-A2.
XX
PD   27-SEP-2001.
XX
PF   23-MAR-2001; 2001WO-US09231.
XX
PR   23-MAR-2000; 2000US-191637P.
PR   11-JUL-2000; 2000US-0614150.
XX
PA   (PEKE ) PE CORP NY.
XX
PI   Venter JC, Adams M, Li PWD, Myers EW;
XX
DR   WPI; [illegible].
DR   N-PSDB; AAB06766.
XX
PT   New isolated nucleic acid detection reagent for detecting 1000 or more
PT   genes in Drosophila and for elucidating cell signalling and cell-cell
PT   interactions.
XX
PS   Claim [illegible]; SEQ ID NO 14781; 21pp + Sequence Listing; English.
XX
CC   The present invention relates to an isolated nucleic acid detection reagent
CC   that is at detecting [illegible] or more genes from Drosophila. The invention is
CC   useful in developmental biology and in elucidating cell signalling and
CC   cell cell interactions in higher eukaryotes for the development of
CC   insecticides, therapeutics and pharmaceutical drugs. The invention
CC   discloses genomic DNA sequences (AAL16129-AAL16511), expressed DNA
CC   sequences (AAL01840-AAL16175) and the encoded proteins
CC   (AAB57737-AAB72072).
CC   The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp://wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence  515 AA;


  Query Match          13.1%;  Score 392.5;  DB 2;  Length 515;
  Best Local Similarity  30.3%;  Pred. No. 1.4e-22;
  Matches  122;  Conservative  58;  Mismatches  125;  Indels  97;  Gaps  13;

Qy      145 [illegible] 196
Db      174 [illegible] 229

Qy      196 [illegible] 251
Db      230 [illegible] 280

Qy      252 [illegible] 311
Db      290 [illegible] 347

Qy      312 [illegible] 368
Db      348 [illegible] 399

Qy      369 [illegible] 414
Db      400 [illegible] 456

Qy      415 [illegible] 474
Db      457 [illegible] 479

Qy      475 [illegible] 516
Db      479 [illegible] 508


RESULT  7
ABB62672
ID   ABB62672 standard; Protein; 515 AA.
XX
AC   ABB62672;
XX
DT   26-MAR-2002  (first entry)
XX
DE   Drosophila melanogaster polypeptide SEQ ID No 14808.
XX
KW   Drosophila; developmental biology; cell signalling; insecticide;
KW   pharmaceutical.
XX
OS   Drosophila melanogaster.
XX
PN   WO200171042-A2.
XX
PD   27-SEP-2001.
XX
PF   23-MAR-2001; 2001WO-US09231.
XX
PR   23-MAR-2000; 2000US-191637P.
PR   11-JUL-2000; 2000US-0614150.
XX
PA   (PEKE ) PE CORP NY.
XX
PI   Venter JC, Adams M, Li PWD, Myers EW;
XX
```

```
DR   WPI; 2001-086860/75.
DR   N-PSDB; ABL46775.
XX
PT   New isolated nucleic acid detection reagent for detecting 1000 or more
PT   genes from Drosophila and for elucidating cell signalling and cell-cell
PT   interactions -
XX
PS   Disclosure; SEQ ID No 14818; 21pp + Sequence Listing; English.
XX
CC   The invention relates to an isolated nucleic acid detection reagent
CC   capable of detecting 1000 or more genes from Drosophila. The invention is
CC   useful in developmental biology and in elucidating cell signalling and
CC   cell cell interactions in higher eukaryotes for the development of
CC   insecticides, therapeutics and pharmaceutical drugs. The invention
CC   discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC   sequences (ABL-16-ABL-175) and the encoded proteins
CC   (ABB57730-ABB72072).
CC   The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence   515 AA;

  Query Match             12.1%;  Score 392.5;  DB 22;  Length 515;
  Best Local Similarity   30.3%;  Pred. No. 1.4e-22;
  Matches  122;  Conservative   58;  Mismatches  125;  Indels   97;  Gaps   13;

Qy        135 KWEVVEP FDFWsIFFR IMKSNQFKEL          VxxWAE   EYLSDKDPQ 195
Db        174 ryeriahldeiqsrhqkrwtlntdasvrtdrlrtllplppderatedlppnecar    e 229

Qy        196 CLIKILPSCLHPYIYRVT---FATANPSSALIIRMENEKGTLKDLIYKAKPKDPMLKKY 251
Db        230 elmellqslhhpyiypvldlatlrssyrvarlvtpfesrqsikdliykaqwnepwarky 289

Qy        252 YNEKKI  TFKL   KTY RQIIEV  K        YC  HA NVMLD   ICRLLDLENSL 310
Db        290 ---rkpnalpvsqqrlarqilealflkerqtplhqhihsqnvilqqaarlsqlenql 347

Qy        311 LGLPSFYRSYFSQFRKINTL  SVDVHCFGHLAYEMIYGRPPDSVPVDSFPPAPSMAVV-  368
Db        348 llssrinavmws rsvteien dvevtqhllyemcfqq-  ----eqttpkpsmrvlem 399

Qy        369 ---            AVIESIT  EAVKNGMPTISRILQMPKESIVLL  SEAAQEKIPTK 414
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Qy        415 LKEALK                            RKEKKILAPKKSKRSALEN 474
Db        457 ikpsl-  -- -- ---       -       --------srstlnlqavkkrqca--- 478

Qy        475 SEEESARYSNSNNSLSGASSPLISPSSPTEPSESGISALPPP 516
Db        479       --  -siqhsseanspetppstphtrrt---qvipap 508


RESULT 8
AAB42077
ID   AAB42077 standard; Protein; 157 AA.
XX
AC   AAB42077;
XX
DT   14-FEB-2001  (first entry)
XX
DE   Human secreted protein BLAST search protein SEQ ID NO: 135.
XX
KW   Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
KW   antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer;
KW   vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic;
KW   cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
KW   neurological disease; infection; human; secreted protein.
XX
OS   Homo sapiens.
XX
PN   WO200058350-A1.
XX
PD   05-OCT-2000.
XX
PF   22-MAR-2000; 2000WO-US07483.
XX
PR   26-MAR-1999;   99US-0126596.
PR   22-DEC-1999;   99US-0171552.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Rosen CA,  Ruben SM,  Komatsoulis G;
XX
DR   WPI; 2000-602357/57.
XX
PT   Nucleic acid molecules encoding human secreted proteins, used in
PT   preventing, treating or ameliorating a disorder, e.g. Alzheimer's and
PT   Parkinson's diseases and cancers
XX
PS   Disclosure; Page 394-395; 423pp; English.
XX
CC   The invention relates to the isolation of genes AAC66410-C66458 encoding
CC   the human secreted proteins AAB42021-B4205 . This sequence represents a
CC   peptide fragment homologous to the protein encoded by the gene given
CC   in the descriptor line. The sequence is a search result from a BLASTX
CC   homology search. The genes and proteins are useful for preventing,
CC   ameliorating or treating medical conditions, e.g. by protein or gene
CC   therapy. The genes are isolated from a range of human tissues disclosed
CC   in the specification. The nucleic acids, proteins, antibodies and
CC   (ant)agonists are useful in the diagnosis, treatment and prevention of:
CC   (a) cancer, e.g. breast and ovarian cancer, and other cancers of the
CC   adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver,
CC   lung, or urogenital; (b) immune disorders e.g. Addison's disease,
CC   allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis,
CC   diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid
CC   arthritis and ulcerative colitis; (c) cardiovascular disorders such
CC   as myocardial ischaemias; (d) wound healing; (e) neurological diseases
CC   e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such
CC   as viral, bacterial, fungal and parasitic infections.
XX
SQ   Sequence   157 AA;

  Query Match             11.1%;  Score 332;  DB 21;  Length 157;
  Best Local Similarity   45.6%;  Pred. No. 1.7e-18;
  Matches   73;  Conservative   28;  Mismatches   51;  Indels    8;  Gaps    4;

Qy        195 QCLIKLLPSCLHPYIYRVT----FATANPSSALIIRMENEKGTLKDLIYKAKPKDPMLKK 250
Db          1 eilmellqslhhpyiypvldlatlrssyrvarlvtpfesrqsikdliykaqwnepwark 60

Qy        251 YCNPKKIQGLELQQIKTYGRQIIEVLKFLHEQGFPYGHLHASNVMLDGDTCRLLDLENS 309
Db         61 y--trkpnalpvsqqrlarqilealflkerqtplhqhihsqnvilqqaarlsqlen 119

Qy        310 LLGLPSFYRSYFSQFRKINTLESVDVHCFGHLLYEMTYGR 349
Db        119 llqlssrinavmws-rsvteienvdivetqhlyemcfq 157


RESULT 9
AAM38834
ID   AAM38834 standard; Protein; 496 AA.
XX
AC   AAM38834;
XX
DT   22-OCT-2001  (first entry)
XX
DE   Human polypeptide SEQ ID NO 1979.
XX
KW   Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
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KW   peripheral nervous system, neuropathy, central nervous system, CNS;
KW   Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW   amyotrophic lateral sclerosis; Shy Drager Syndrome; chemotactic;
KW   chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW   leukaemia.
XX
OS   Homo sapiens.
XX
PN   WO200153312-A1.
XX
PD   26-JUL-2001.
XX
PF   26-DEC-2000; 2000WO-US34263.
XX
PR   21-JAN-2000; 2000US-0488725.
PR   25-APR-2000; 2000US-0552317.
PR   09-JUL-2000; 2000US-0598042.
PR   19-JUL-2000; 2000US-0620312.
PR   03-AUG-2000; 2000US-0653450.
PR   14-SEP-2000; 2000US-0662191.
PR   19-OCT-2000; 2000US-0693036.
PR   29-NOV-2000; 2000US-0727344.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Tang YT,  Liu C,  Asundi V,  Chen R,  Ma Y,  Qian XB,  Ren F,  Wang D;
PI   Wang J,  Wang Z,  Wehrman T,  Xu C,  Xue AJ,  Yang Y,  Zhang J;
PI   Zhao QA,  Zhou P,  Goodrich R,  Drmanac RT;
XX
DR   WPI; 2001-442253/47.
DR   N-PSDB; AAI59776.
XX
PT   Novel nucleic acids and polypeptides, useful for treating disorders
PT   such as central nervous system injuries -
XX
PS   Example 2; SEQ ID NO 5551; 10078pp; English.
XX
CC   The invention relates to human nucleic acids (AAI57798-AAI61369) and
CC   the encoded polypeptides (AAM38642-AAM42213) with nootropic,
CC   immunosuppressant and cytostatic activity. The polynucleotides are useful
CC   in gene therapy. A composition containing a polypeptide or polynucleotide
CC   of the invention may be used to treat diseases of the peripheral nervous
CC   system such as peripheral nervous injuries, peripheral neuropathy and
CC   localised neuropathies and central nervous system diseases, such as
CC   Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC   lateral sclerosis, and Shy Drager Syndrome. Other uses include the
CC   utilisation of the activities such as: immune system suppression,
CC   activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC   and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC   receptor/receptor activity, arthritis and inflammation, leukaemias and
CC   CNS disorders.
CC   Note: The sequence data for this patent did not form part of the printed
CC   specification.
XX
SQ   Sequence   496 AA;

  Query Match             7.1%;  Score 212.5;  DB 22;  Length 496;
  Best Local Similarity   21.4%;  Pred. No. 2.4e-08;
  Matches   67;  Conservative   85;  Mismatches  179;  Indels   93;  Gaps   19;

Qy    [illegible] IVE[illegible]AA[illegible]LA[illegible]HEY[illegible]EV[illegible]VENGW[illegible]VERYS[illegible]LLNN[illegible]  [illegible]IAGLSLP 74
Db    [illegible]pdd[illegible]kkk[illegible]yk[illegible]   [illegible]sewt[illegible]ry[illegible]dklyn[illegible]kkqtpamalk 71

Qy    [illegible] EEEKK[illegible]NM[illegible]AE[illegible]K[illegible]NYENV[illegible]NH[illegible]N[illegible]LVKKPL            [illegible] 120
Db    [illegible] pdl[illegible]qlrv[illegible]ypelyn[illegible]atlqmdspklhqsdpsed 131

Qy    121 ENNYSANY[illegible]AL[illegible]VSMEEK[illegible]   EWEVVLE[illegible]            WK[illegible]KEEY[illegible]MK 167
Db    132 [illegible]pklhst[illegible]qnin[illegible]qpsqnphakp[illegible]lkviqkqstqkv[illegible]ak[illegible]qktyek 191

Qy    168 IKNQPKEEVESWA[illegible]KYLSDKE[illegible]KLLLSCLHPYIYRVIFAIANESSALLIRM 227
Db    192 [illegible]qkkivlark[illegible]qkhirs[illegible]      [illegible]kpllqlty[illegible]klyfeld 241

Qy    229 FNEK[illegible]EKEKKY[illegible]KIY[illegible]EVLEELHEKGEPYG 287
Db    242 fqyqqel -----  --    -  [illegible]hlqrerstpehrartyaaelasalaylhsikivyr 285

Qy    288 HLHASNVMLDG          DICK     LLELENSLLGLESPYRSYPSQPEKINILESVD 334
Db    286 dlkpenillds[illegible]qhvvltdfqlckeqiaisdt[illegible]tcqtpeylap[illegible]rkqpydnt[illegible]d 34[illegible]

Qy    335 VHCFGHLLYEMIYGRPP            DSV    PVDSPFPAPSMAVVAVLESILSCEACK 381
Db    344 wwelqavlyemlyglppfyerdvaemydnilhkpl-slrpqvstlawsileellekdr-q 401

Qy    382 NGMPTISRLLQM---PLFSDVLLTTSEKPQEKIP 412
Db    402 nrlqake[illegible]f[illegible]iqhpff[illegible]  [illegible]lswafl[illegible]qkkip 433


RESULT 10
AAM40620
ID   AAM40620 standard; Protein; 496 AA.
XX
AC   AAM40620;
XX
DT   22-OCT-2001  (first entry)
XX
DE   Human polypeptide SEQ ID NO 5551.
XX
KW   Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW   peripheral nervous system, neuropathy, central nervous system, CNS;
KW   Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW   amyotrophic lateral sclerosis; Shy Drager Syndrome; chemotactic;
KW   chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW   leukaemia.
XX
OS   Homo sapiens.
XX
PN   WO200153312-A1.
XX
PD   26-JUL-2001.
XX
PF   26-DEC-2000; 2000WO-US34263.
XX
PR   21-JAN-2000; 2000US-0488725.
PR   25-APR-2000; 2000US-0552317.
PR   09-JUL-2000; 2000US-0598042.
PR   19-JUL-2000; 2000US-0620312.
PR   03-AUG-2000; 2000US-0653450.
PR   14-SEP-2000; 2000US-0662191.
PR   19-OCT-2000; 2000US-0693036.
PR   29-NOV-2000; 2000US-0727344.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Tang YT,  Liu C,  Asundi V,  Chen R,  Ma Y,  Qian XB,  Ren F,  Wang D;
PI   Wang J,  Wang Z,  Wehrman T,  Xu C,  Xue AJ,  Yang Y,  Zhang J;
PI   Zhao QA,  Zhou P,  Goodrich R,  Drmanac RT;
XX
DR   WPI; 2001-442253/47.
DR   N-PSDB; AAI59776.
XX
PT   Novel nucleic acids and polypeptides, useful for treating disorders
PT   such as central nervous system injuries -
XX
PS   Example 2; SEQ ID NO 5551; 10078pp; English.
XX
CC   The invention relates to human nucleic acids (AAI57798-AAI61369) and
CC   the encoded polypeptides (AAM38642-AAM42213) with nootropic,
CC   immunosuppressant and cytostatic activity. The polynucleotides are useful
CC   in gene therapy. A composition containing a polypeptide or polynucleotide
```

```
CC   of the invention may be used to treat diseases of the peripheral nervous
CC   system, such as peripheral nervous injuries, peripheral neuropathy and
CC   localised neuropathies and central nervous system diseases, such as
CC   Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC   lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC   utilisation of the activities such as: immune system suppression,
CC   [illegible] activity, haemostatic
CC   and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC   assays for receptor activity, arthritis and inflammation, leukaemias and
CC   C.N.S disorders.
CC   Note: The sequence data for this patent did not form part of the printed
CC   specification.
XX
SQ   Sequence   496 AA;

  Query Match             7.%;  Score 211.5;  DB 22;  Length 496;
  Best Local Similarity   21.4%;  Pred. No. 2.8e-08;
  Matches   97;  Conservative   85;  Mismatches  179;  Indels   93;  Gaps   19;

Qy         17 IVPLTAAIFASQSLQSHIFYIIRVQRGISVENSWQIVRRYSDFDLLNNSL--QIAGLSLP 74
Db         15 svsipssdehrokkkrttvykvlvev    rsewtvrryset[illegible] 71
Qy         75 LPPKKLIGNMDREFIAERQKGLQNYLNVITTNHILSNCELVKKFL           E 120
Db         72 ipakritqdhtdpdtikqrradlnetiqelvrypelynhpdvratlqmdspkhqsdpsed 131
Qy        121 PNNYSANYTEIALQQVSMFFRSEP  KWEVVEIIKDIG-----------WRIRKKYFLMK 167
Db        132 edersspqklhstsqnlnlqpsarphakp[illegible] 191
Qy        168 IKNQPKERLVLSWALEQPPKYLSDKDPQ[illegible]PVTFAYANESSALLIRM 227
Db        192 vl---qkkiv[illegible] 241
Qy        228 FNEKGILKELLIYEAKEKPPEIFKY[illegible]LFKLHERGFYG 287
Db        242 fvnqqel---------------tfhlqrerstpehrartyaaeiasalgylhsikivyr 285
Qy        288 HLHASNVMLDG      DFCR   LLD ENSLLGLPSFYRSYFSQFRKINTLESVD 334
Db        286 dlkpenilldsvgh[illegible]frqkeqaladtttftrptpeylap  evlrkqpydntvd 343
Qy        335 VHCFGHLLYEMTYGRPP---       ISV   PVDSFPPAPSMAVVAVLESTLSCEACK 381
Db        344 wwclqavlyemlyqippftyerdvaemydnilhkpl-slrpqvsltawsilqellokdr-q 401
Qy        382 NGMPLISK LQM   PLFSDVLLIISEKPQFKIP 412
Db        402 nrlqakedflelqnhpffesiswadlvqkkip 433

RESULT 11
AAW87772
ID   AAW87772 standard; Protein; 496 AA.
XX
AC   AAW87772;
XX
DT   17 MAR 1999  (first entry)
XX
DE   Human serum glucocorticoid regulated kinase (H-SGK2) polypeptide.
XX
KW   Serum glucocorticoid regulated kinase; H-SGK2; human; gene therapy;
KW   serine/threonine protein kinase; inflammation; rheumatoid arthritis;
KW   septicaemia; autoimmune disease; inflammatory bowel disease; psoriasis;
KW   transplant rejection; infection; stroke; ischaemia; renal disorder;
KW   restenosis; brain injury; acquired immune deficiency syndrome; AIDS;
KW   metabolic bone; osteoporosis; lymphoproliferation; atherosclerosis;
KW   Alzheimer's disease; cancer.
XX
OS   Homo sapiens.
XX
PN   EP889127-A1.
XX
PD   07-JAN-1999.
XX
PF   18-JUN-1998;   98EP-0304830.
XX
PR   23-DEC-1997;   97US-0997212.
PR   01-JUL-1997;   97US-0051446.
XX
PA   (SMIK ) SMITHKLINE BEECHAM CORP.
XX
PI   Kumar S,  Zou C;
XX
DR   WPI; 1999-062658/06.
DR   N-PSDB; AAV99653.
XX
PT   New nucleic acid encoding human H-SGK2 poly peptide(s) - useful for
PT   diagnosis, treatment and prevention of e.g. arthritis, infections,
PT   cancer, Alzheimer's disease
XX
PS   Claim 11; Page 8; 27pp; English.
XX
CC   This represents a human serum glucocorticoid regulated kinase (H-SGK2)
CC   polypeptide, a novel member of the serine/threonine protein kinase
CC   family. A host cell transfected or transformed with an expression system
CC   comprising the H-SGK2 nucleic acid can be used for the recombinant
CC   production of the protein. The H-SGK2 polypeptide is useful for treating
CC   a subject who require enhanced/reduced activity or expression/inhibition
CC   of the polypeptide. Recombinant H-SGK2 is used to raise antibodies; in
CC   vaccines; in drug screens; and to identify soluble or membrane-bound
CC   receptors. The H-SGK2 polypeptide [illegible] inflammation
CC   (rheumatoid arthritis); septicaemia; autoimmune disease (inflammatory
CC   bowel disease or psoriasis); transplant rejection; infection; stroke;
CC   ischaemia; renal disorders; restenosis; brain injury; acquired immune
CC   deficiency syndrome; metabolic bone diseases (osteoporosis);
CC   cancer (e.g. lymphoproliferation); atherosclerosis and Alzheimer's
CC   disease. The H-SGK2 nucleic acids can be used in gene therapy
XX
SQ   Sequence   496 AA;

  Query Match             6.8%;  Score 205.5;  DB 20;  Length 496;
  Best Local Similarity   21.1%;  Pred. No. 8.4e-04;
  Matches   96;  Conservative   85;  Mismatches  18[illegible];  Indels   93;  Gaps   19;

Qy         17 IVPLTAAIFASQSLQSHIFYIIRVQRGI[illegible]NSWQIVRRYSDFDLLNNSL--QIAGLSLP 74
Db         15 svsipssdehrokkkrttvykvlvev    rsewtvrryset[illegible]kkqtpamilk 71
Qy         75 LPPKKLIGNMDREFIAERQKGLQNYLNVITTNHILSNCELVKKFL           E 120
Db         72 ipakritqdhtdpdtikqrradlnetiqelvrypelynhpdvratlqmdspkhqsdpsed 131
Qy        121 PNNYSANYTEIALQQVSMFFRSEP  KWEVVEIIKDIG           WRIRKKYFLMK 167
Db        132 edersspqklhstsqnlnlqpsarphakp[illegible] 191
Qy        168 IKNQPKERLVLSWALEQPPKYLSDKDPQ[illegible]PVTFAYANESSALLIRM 227
Db        192 vl---qkkiv[illegible] 241
Qy        228 FNEKGILKELLIYEAKEKPPEIFKY[illegible]GFYG 287
Db        242 fvnqqel---------------tfhlqrerstpehrartyaaeiasalgylhsikivyr 285
Qy        288 HLHASNVMLDG      DFCR   [illegible]NTLESVD 334
Db        286 dlkpenilldsvghvvltdfglckeala[illegible]evlrkqpydntvd 343
Qy        335 VHCFGHLLYEMTYGRPP---       ISV   PVDSFPPAPSMAVVAVLESTLSCEACK 381
Db        344 wwclqavlyemlyqippftyerdvaemydnilhkpl-slrpqvsltawsilqellokdr-q 401
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Qy    392 NIMPLIGRLIQM    PLESDVLLITSEKPQFKIP 412
                 ::         |: ::  | |||
Db    402 rrllakedtlerqnhpttes   lswadlvqkkip 433
```

RESULT 12
AAY5[illegible]
ID AAY5[illegible] standard; Protein; 912 AA.
XX
AC AAY5[illegible];
XX
DT 18-FEB-2000 (first entry)
XX
DE Human GEK2 protein.
XX
KW Antirheumatic; antiathritic; antiinflammatory; antiallergic; osteopathic;
KW antipsoriatic; antiarterosclerotic; antiasthmatic; immunosupressive;
KW neuroprotective; cardiant; cerebroprotective; cytostatic; antidiabetic;
KW vulnery; STE20 protein kinase; STLK2; STLK3; STLK4; STLK5; STLK6; STLK7;
KW ZC1; ZC2; ZC3; ZC4; KHS2; SULU1; SULU3; GEK2; PAK4; PAK5; antagonist;
KW antibody; gene therapy; rheumatoid arthritis; artherosclerosis; asthma;
KW inflammatory bowel disease; Crohn's disease; osteoarthritis; psoriasis;
KW rhinitis; autoimmunity; organ transplantation; multiple sclerosis;
KW myocardial infarction; cardiovascular disease; stroke; renal failure;
KW oxidative stress related neurodegenerative disorder; Parkinson's disease;
KW amylotrophic lateral sclerosis; Leigh syndrome; cancer; cardiomyopathy;
KW ischemic disorder; inflammation; diabetes mellitus; fibrosis; mitosis;
KW mesangial disorder; growth regulation; wound healing; T cell activation;
KW immunosuppressant.
XX
OS Homo sapiens.
XX
PN WO9953036-A2.
XX
PD 21-OCT-1999.
XX
PF 13-APR-1999; 99WO-US08150.
XX
PR 14-APR-1998; 98US-0081784.
XX
PA (SUGE-) SUGEN INC.
XX
PI Plowman G, Martinez R, Whyte D;
XX
DR WPI; 1999-611[illegible]/52.
DR N-PSDB; AAZ4[illegible].
XX
PT Novel kinase related polypeptides used for the diagnosis and treatment
PT of kinase related diseases and disorders
XX
PS Disclosure; Page 432-506; 587pp; English.
XX
CC This sequence represents a novel STE20 related protein kinase. The
CC invention relates to nucleic acid molecule encoding a kinase polypeptide
CC selected from STLK2, STLK3, STLK4, STLK5, STLK6, STLK7, ZC1, ZC2, ZC3,
CC ZC4, KHS2, SULU1, SULU3, GEK2, PAK4 and PAK5. The proteins are used to
CC identify agonists and antagonists, and to raise antibodies. The
CC polynucleotides are useful in gene therapy protocols.The polynucleotides,
CC polypeptides, antibodies, antagonists and agonists may be used to treat
CC diseases such as immune related disorders and diseases (e.g. rheumatoid
CC arthritis, artherosclerosis, chronic inflammatory bowel disease (e.g.
CC Crohn's disease), asthma, osteoarthritis, psoriasis, atherosclerosis,
CC rhinitis, autoimmunity, and organ transplantation, chronic inflammatory
CC pelvic disease, multiple sclerosis, organ transplantation, myocardial
CC infarction, cardiovascular disease, stroke, renal failure, oxidative
CC stress related neurodegenerative disorders (e.g. amylotrophic lateral
CC sclerosis, Parkinson's disease and Leigh syndrome), cancer,
CC cardiomyopathies, ischemic disorders, inflammatory disorders, diabetes
CC mellitus, fibrotic and mesangial disorders. The proteins may also be
CC useful for cell growth regulation (e.g. in wound healing), T cell
CC activation, mitosis control, and as immunosuppressants
XX
SQ Sequence 912 AA;

```
  Query Match             6.6%;  Score 199.5;  DB 20;  Length 912;
  Best Local Similarity   24.2%;  Pred. No. 5.8e-07;
  Matches  123;  Conservative   69;  Mismatches  184;  Indels  141;  Gaps   25;

Qy    113 ELVEKELPPNNYSANYSEIAQQVSMEEPSEPKWEVVPELEDIGWRIEKKKYPLMKIKNQF 172
            | |: ||||                           ||:|  | |      | |    | ||
Db     24 ehvrrldpaew  -  -          -   -   -weirqelqd-qatqkqy    kakn    55

Qy    173 KERLVLSWAPLGPDKYLSD-KEF-LIKLLIPCLHPYIYRVIAIANECALLIRMPNEK 231
           ||   |: |: |      |     : :|:    |::| :| ||||  :|   |  ::     :
Db     56 ketqalaaakr-e-tksccqdfyleel-ie-rpyleq-nyyhfikwimietepa 115

Qy    232 GIAEILIIRAEER-PLEEY-NSEKL-LL-L-VS-L-VYV-RLKQIGHLHA 291
           | :  :: :                 :||   ||:    ||:|| | ||| |     :  | |
Db    116 qavdaimleld-  --              rslteqsiqpvrcpdeaetthskrilhrdlka 160

Qy    292 SNVM  LLRR            IPSLLSLNSSSPSPRSLSQEERNTIA         332
             ||:  |:||                 :  |     :| :| | :      :        |::
Db    161 qnvlmtleqdirladfqvsaknlktlqkrdstiatpywmapevvmcetmkdtpydyk 217

Qy    333 VDVHCFGHLLYEMTYGRPP  LSVPV         LSFPP    APSMAVVAVLESILSCEAC 380
            |:   |  | |   ||  |:    |:                 | ||     ||    |       |
Db    218 adiwslgitliemaqleppheinpmrvllkiakdppttlltpskwsve frdflklald 276

Qy    381 KN--GMPTISELLQMPLFSPVLLTSPEPQ---PTEKEALRIAKEIEKKLLSLQKQIH 438
           ||     |: :::|: ;  | :    | |                |||     |: :  ::   :
Db    277 kneetrpsaaqllehpfvssi    tsnk          al:    elvaeakaemeele 319

Qy    439 QHRPITPAQSHPCSPPPPPKKPILAPKKS--SAL-NSPFFSARYSNSNNSGSGASSPL I 497
            |            | ||:             | ||   ::|: | :        | :|
Db    320 dqr        deqeed            avdaastlenhtqnsssvspps    lnadkplee 360

Qy    498 SPSSPTPPS--------------TSGISALPPPPPPPPPPP---     AAPLP -  -PASTEV 534
           |||:|  ||                    || :|   ||     |            | |:|      | | :
Db    361 spstplapsqsqdsvnepcsqpsdrslqttsppvvapanealavpvplrksrpvsmda 420

Qy    535 PAQLSSQAVNGMSRGALLSSIQNFQKGT 562
            |:: :            | |  :    || :
Db    421 riqvaqekqvaeqgqdlspaanrsqkas 448
```

RESULT 13
AAY55966
ID AAY55966 standard; Protein; 968 AA.
XX
AC AAY55966;
XX
DT 18-FEB-2000 (first entry)
XX
DE Full length human GEK2 protein.
XX
KW Antirheumatic; antiathritic; antiinflammatory; antiallergic, osteopathic;
KW antipsoriatic; antiarterosclerotic; antiasthmatic; immunosupressive;
KW neuroprotective; cardiant; cerebroprotective; cytostatic; antidiabetic;
KW vulnery; STE20 protein kinase; STLK2; STLK3; STLK4; STLK5; STLK6; STLK7;
KW ZC1; ZC2; ZC3; ZC4; KHS2; SULU1; SULU3; GEK2; PAK4; PAK5; antagonist;
KW antibody; gene therapy; rheumatoid arthritis; artherosclerosis; asthma;
KW inflammatory bowel disease; Crohn's disease; osteoarthritis; psoriasis;
KW rhinitis; autoimmunity; organ transplantation; multiple sclerosis;
KW myocardial infarction; cardiovascular disease; stroke; renal failure;
KW oxidative stress-related neurodegenerative disorder; Parkinson's disease;
KW amylotrophic lateral sclerosis; Leigh syndrome; cancer; cardiomyopathy;
KW ischemic disorder; inflammation; diabetes mellitus; fibrosis; mitosis;
KW mesangial disorder; growth regulation; wound healing; T cell activation;
KW immunosuppressant.
XX
OS Homo sapiens.
XX
PN WO9953036-A2.
XX
PD 21-OCT-1999.

```
XX
PR   1 -APR-1999;   99WO-US0815[illegible].
XX
PR   14-APR-1998;   98US-0081784
XX
PA   (SUGE-) SUGEN INC.
XX
PI   Plowman G,  Martinez R,  Whyte D.
XX
DR   WPI; 1999-611301/52.
DR   N-PSDB; AAZ4054.
XX
PT   Novel kinase-related polypeptides used for the diagnosis and treatment
PT   of kinase-related diseases and disorders -
XX
PS   Claim 11; Page 375-378; 497pp; English.
XX
CC   This sequence represents a novel STE20-related protein kinase. The
CC   invention relates to nucleic acid molecule encoding a kinase polypeptide
CC   selected from [illegible]
CC   [illegible], KHS2, SULU1, SULU3, GEK2, PAK4 and PAK5. The proteins are used to
CC   identify agonists and antagonists, and to raise antibodies. The
CC   polynucleotides are useful in gene therapy protocols. The polynucleotides,
CC   polypeptides, antibodies, antagonists and agonists may be used to treat
CC   diseases such as immune-related disorders and diseases (e.g. rheumatoid
CC   arthritis, arteriosclerosis, chronic inflammatory bowel disease (e.g.
CC   Crohn's disease), asthma, osteoarthritis, psoriasis, atherosclerosis,
CC   rhinitis, autoimmunity, and organ transplantation, chronic inflammatory
CC   pelvic disease, multiple sclerosis, organ transplantation, myocardial
CC   infarction, cardiovascular disease, stroke, renal failure, oxidative
CC   stress related neurodegenerative disorders (e.g. amyotrophic lateral
CC   sclerosis, Parkinson's disease and Leigh syndrome), cancer,
CC   cardiomyopathies, ischemic disorders, inflammatory disorders, diabetes
CC   mellitus, fibrotic and mesangial disorders. The proteins may also be
CC   useful for cell growth regulation (e.g. in wound healing), T cell
CC   activation, mitosis control, and as immunosuppressants.
XX
SQ   Sequence   968 AA;

  Query Match              6.6%;  Score 199.5;  DB 20;  Length 968;
  Best Local Similarity   21.2%;  Pred. No. 6.3e-07;
  Matches  [illegible];  Conservative   66;  Mismatches  134;  Indels  141;  Gaps   25;

Qy        11[illegible] EIVKK[illegible]NNY[illegible]LMKIFNQP 172
Db         24 [illegible]dldp[illegible] -we[illegible]vqelqd-qatakvy---kak[illegible] 5[illegible]

Qy        17[illegible] K[illegible]SWA[illegible]EPVIVEVTIATANP[illegible]ALLIEMPNEK 2[illegible]
Db         5[illegible] [illegible]dpyirk[illegible]klwimie[illegible] 115

Qy        23[illegible] [illegible]EVIEEI[illegible]HA 2[illegible]
Db        116 [illegible]----------------[illegible]ka 1[illegible]

Qy        2[illegible] SNVM[illegible] -----I[illegible]RLLELENSILALESFYRSYESQFRKINIIF------S 332
Db        1[illegible] [illegible]dir[illegible]itavsak[illegible] 217

Qy        3[illegible] VIVH[illegible]SVIV [illegible]----A[illegible]SMAVVAV[illegible]SCFA[illegible] 3[illegible]
Db        21[illegible] [illegible]dlws[illegible]iemaqiepphhe[illegible]klne[illegible]dppt[illegible]tpskws[illegible]kiaid 276

Qy        [illegible]FEIIEEIKEALRIAKEQIEKRLIEEQKCIH 438
Db        2[illegible] knpetrpsaaqllqhpfvs[illegible]tank [illegible]alr[illegible]elv[illegible]akaevmeeie 319

Qy        4[illegible] [illegible]NCNN[illegible]SCA[illegible] 4[illegible]
Db        [illegible] d[illegible] -deqeeed------- avq[illegible]s[illegible]tqns[illegible]pps [illegible] [illegible]

Qy        4[illegible] SPSSPIFPS- -  [illegible]SGISALIPPPPLPPP- ----AAPIP ----PASTPV 5[illegible]
Db        361 spstplapsqsqdsvnepesqpsqdrs[illegible]qttsppv[illegible]lavpv[illegible]ksrpvsmda 42[illegible]

Qy        5[illegible] PAC[illegible]S[illegible]QAVNCM[illegible]CA[illegible]NE[illegible]K[illegible] 562
Db        421 riqvaqokqvaeqqqdlspaan[illegible]sqk[illegible] 44[illegible]


RESULT  14
AAY93499
ID   AAY93499 standard; Protein; 1081 AA.
XX
AC   AAY93499;
XX
DT   25-SEP-2000  (first entry)
XX
DE   Amino acid sequence of the protein kinase Fkh2 polypeptide.
XX
KW   Protein kinase, Fkh1, Fkh2, Ypk1, Yrk2, protein kinase B-alpha;
KW   human serum and glucocorticoid induced protein kinase; SGK; PKBalpha;
KW   3 phosphoinositide-dependent protein kinase 1; PDK1; fungal infection;
KW   thrush; cancer; diabetes; obesity; antifungal; Candida infection.
XX
OS   Saccharomyces cerevisiae.
XX
PN   WO200036135-A2.
XX
PD   22-JUN-2000.
XX
PF   14-DEC-1999;   99WO-GB04228.
XX
PR   14-DEC-1998;   98US-0112134.
XX
PA   (MEDI-) MEDICAL RES COUNCIL.
PA   (REGC ) UNIV CALIFORNIA.
XX
PI   Thorner JW,  Alessi DR,  Torrance PD,  Casamayor A;
XX
DR   WPI; 2000-442391/38.
DR   N-PSDB; AAA46567.
XX
PT   Screening method identifying compounds which modulate protein kinase
PT   activity for use in treating fungal infections and cancer
XX
PS   Disclosure; Page 17-18; 15[illegible]pp; English.
XX
CC   The present sequence represents a protein kinase Fkh2. The specification
CC   describes a screening method to identify a compound which modulates the
CC   activity of protein kinases from different [illegible] in host yeast
CC   cells. The method is used to identify a compound which modulates
CC   (inhibits) the activity of a protein kinase. Fkh1 or Fkh2 phosphorylate
CC   and activate Ypk1, Yrk2, human serum and glucocorticoid induced protein
CC   kinase (SGK) or protein kinase B-alpha (PKBalpha). 3-phosphoinositide
CC   dependent protein kinase-1 (PDK1) is used to phosphorylate and activate
CC   Ypk1 and Yrk2 or SGK but not PKBalpha or p70S6 kinase. Compounds
CC   identified by the methods are used to treat fungal infections e.g.
CC   thrush, and to treat cancer. To treat cancer, the compounds inhibit PKB,
CC   PDK1 or the activation of PKB by PDK1. Compounds which activate PKB or
CC   PDK1 can be used in the treatment of diabetes or obesity, and compounds
CC   which inhibit a fungal functional homologue of PDK1 (Fkh1 or Fkh2) or
CC   SGK (Ypk1 or Yrk2) can be used as an antifungal agent to treat Candida
CC   infections, e.g. thrush.
XX
SQ   Sequence   1081 AA;

  Query Match              6.5%;  Score 19[illegible];  DB 2[illegible];  Length 1081;
  Best Local Similarity   21.4%;  Pred. No. 1.7e-06;
  Matches  10[illegible];  Conservative   74;  Mismatches  1[illegible];  Indels  144;  Gaps   20;

Qy        161 [illegible]MK[illegible]VI[illegible]WA[illegible]VTPATANES 220
Db        2[illegible] [illegible]leyl[illegible] [illegible]tqdes 251
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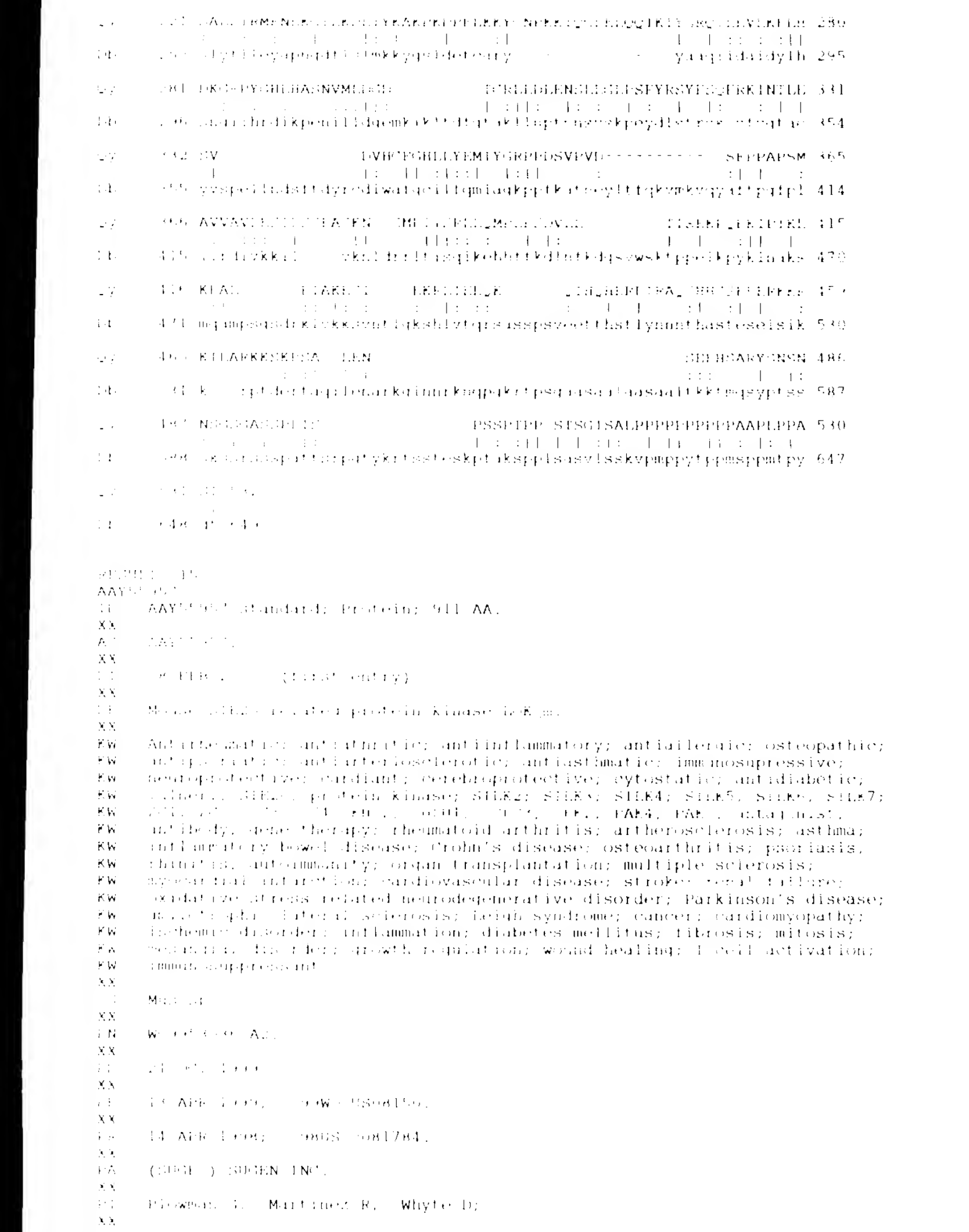

DR WPI; 1999-611301/52.
XX
PT Novel kinase-related polypeptides used for the diagnosis and treatment
PT of kinase related diseases and disorders
XX
PS Disclosure; Page 350 353; 387pp; English.
XX
CC This sequence represents a novel PTP22 related protein kinase. The
CC invention relates to nucleic acid molecule encoding a kinase polypeptide
CC selected from SILK2, SILK3, SILK4, SILK5, SILK6, SILK7, ZC1, ZC2, ZC3,
CC ZC4, KHS2, SULU1, SULU3, GEK2, PAK4 and PAK5. The proteins are used to
CC identify agonists and antagonists, and to raise antibodies. The
CC polynucleotides are useful in gene therapy protocols.The polynucleotides,
CC polypeptides, antibodies, antagonists and agonists may be used to treat
CC diseases such as immune-related disorders and diseases (e.g. rheumatoid
CC arthritis, artherosclerosis, chronic inflammatory bowel disease (e.g.
CC Crohn's disease), asthma, osteoarthritis, psoriasis, atherosclerosis,
CC sinusitis, autoimmunity, and organ transplantation, chronic inflammatory
CC pelvic disease, multiple sclerosis, organ transplantation, myocardial
CC infarction, cardiovascular disease, stroke, renal failure, oxidative
CC stress-related neurodegenerative disorders (e.g. amylotrophic lateral
CC sclerosis, Parkinson's disease and Leigh syndrome), cancer,
CC cardiomyopathies, ischemic disorders, inflammatory disorders, diabetes
CC mellitus, fibrotic and mesangial disorders. The proteins may also be
CC useful for cell growth regulation (e.g. in wound healing), T cell
CC activation, mitosis control, and as immunosuppressants.
XX
SQ Sequence 911 AA;

Query Match 6.0%; Score 180.5; DB 20; Length 911;
Best Local Similarity 24.8%; Prob. No. 1.8e-05;
Matches 116; Conservative 55; Mismatches 172; Indels 125; Gaps 22;

Search completed: June 12, 2002, 09:55:47
Job time: 123 sec

OM protein - protein search, using sw model

Run on: June 12, 2002, 09:53:49 ; Search time 65.66 Seconds
(without alignments)
214.645 Million cell updates/sec

Title: US-09-684-458-2
Perfect score: 3001
Sequence: 1 MAEMEKEFASKVI [illegible] .........EQKGLESAKIPDESAFKIG 577

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 241628 seqs, 44425594 residues

Total number of hits satisfying chosen parameters: 241628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: Issued_Patents_AA:*
1: [illegible]_COMB.pep:*
2: [illegible]_COMB.pep:*
3: [illegible]_COMB.pep:*
4: [illegible]_COMB.pep:*
5: [illegible]_COMB.pep:*
6: [illegible]backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	152.5	5.1	1297	2	US-08-290-731C-4	Sequence 4, Appli
2	145	4.8	676	1	US-09-313-530-2	Sequence 2, Appli
3	144	4.8	1255	1	US-08-467-083-68	Sequence 68, Appl
4	144	4.8	1255	1	US-08-414-417B-68	Sequence 68, Appl
5	144	4.8	1255	2	US-08-484-438-8	Sequence 8, Appli
6	144	4.8	1255	2	US-08-486-343A-68	Sequence 68, Appl
7	144	4.8	1255	2	US-08-625-101-2	Sequence 2, Appli
8	144	4.8	1255	2	US-08-468-545B-68	Sequence 68, Appl
9	144	4.8	1255	2	US-08-356-786-2	Sequence 2, Appli
10	144	4.8	1255	3	US-09-464-580B-68	Sequence 68, Appl
11	142	4.7	426	2	US-08-852-743-2	Sequence 2, Appli
12	142	4.7	426	2	US-09-21[illegible]-930-4	Sequence 4, Appli
13	142	4.7	426	3	US-09-340-993-4	Sequence 4, Appli
14	142	4.7	426	3	US-09-185-370-2	Sequence 2, Appli
15	142	4.7	426	4	US-09-152-406-4	Sequence 4, Appli
16	142	4.7	426	4	US-09-468-442-4	Sequence 4, Appli
17	141.5	4.7	431	4	US-09-152-406-3	Sequence 3, Appli
18	141	4.7	403	2	US-08-712-709-3	Sequence 3, Appli
19	141	4.7	403	3	US-09-111-414-3	Sequence 3, Appli
20	141	4.7	403	4	US-09-541-228-3	Sequence 3, Appli
21	138	4.6	652	1	US-08-318-831-8	Sequence 8, Appli
22	137.5	4.6	431	2	US-09-211-930-5	Sequence 5, Appli
23	137.5	4.6	431	3	US-09-340-993-5	Sequence 5, Appli
24	137.5	4.6	431	4	US-09-468-442-5	Sequence 5, Appli
25	136.5	4.5	580	1	US-08-414-417B-69	Sequence 69, Appl
26	136.5	4.5	580	2	US-08-486-348A-69	Sequence 69, Appl
27	136.5	4.5	580	2	US-08-468-545B-69	Sequence 69, Appl
28	136.5	4.5	580	3	US-[illegible]	Sequence 69, Appl
29	134	4.5	1315	3	US-08-899-[illegible]-3	Sequence 3, Appli
30	133	4.4	416	2	US-09-211-930-3	Sequence 3, Appli
31	133	4.4	416	3	US-09-340-993-3	Sequence 3, Appli
32	133	4.4	416	4	US-09-468-442-3	Sequence 3, Appli
33	133	4.4	694	3	US-[illegible]A-[illegible]	Sequence [illegible], Appl
34	133	4.4	1248	2	US-[illegible]-2	Sequence 2, Appli
35	133	4.4	1248	4	US-[illegible]	Sequence 2, Appli
36	132.5	4.4	947	2	US-[illegible]887-[illegible]-2	Sequence 2, Appli
37	132.5	4.4	947	2	US-[illegible]	Sequence 2, Appli
38	132.5	4.4	947	2	US-[illegible]	Sequence 2, Appli
39	132.5	4.4	947	4	US-[illegible]	Sequence 1, Appli
40	131	4.4	1255	2	US-[illegible]-4	Sequence 4, Appli
41	131	4.4	1255	3	US-[illegible]-1	Sequence 1, Appli
42	131	4.4	1255	4	US-[illegible]-4	Sequence 4, Appli
43	130	4.3	416	2	US-09-211-930-11	Sequence 11, Appl
44	130	4.3	416	3	US-09-340-993-11	Sequence 11, Appl
45	130	4.3	416	4	US-09-468-442-11	Sequence 11, Appl

ALIGNMENTS

RESULT 1
US-08-290-731C-4
; Sequence 4, Application US/08290731C
; Patent No. 5843646
; GENERAL INFORMATION:
; APPLICANT: BOWTELL, David Douglas Lawrence
; TITLE OF INVENTION: DNA MOLECULES ENCODING MURINE
; TITLE OF INVENTION: [illegible]
; TITLE OF INVENTION: AND [illegible] POLYPEPTIDES
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: [illegible], MACPEAK & SEAS
; STREET: [illegible] PENNSYLVANIA AVENUE N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/290,731C
; FILING DATE: 17 OCT 1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/AU93/00068
; FILING DATE: 17-FEB-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PL0921/92
; FILING DATE: 17-FEB-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: KIT, Gordon
; REGISTRATION NUMBER: 30,764
; REFERENCE/DOCKET NUMBER: Q-36066
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 293-7060
; TELEFAX: (202) 293-7860
; TELEX: 6491103
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1297 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-290-731C-4

Query Match 5.1%; Score 152.5; DB 2; Length 1297;

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  Best Local Similarity   22.5%;  Pred. No. 0.00061;
  Matches [illegible];  Conservative   68;  Mismatches  227;  Indels  177;  Gaps   35;

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Db     [illegible] [illegible] 77[illegible]

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Db     [illegible] [illegible] ERKKE 862

Qy     1[illegible] [illegible]KYLSDKE[illegible]LIKLLP[illegible]LHPY  IYRVIFATANESSALLIRMFNE 230
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Qy     27[illegible] [illegible] 336
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Qy     33[illegible] [illegible]YEMIY[illegible]SVPVL[illegible]AFSMAVVA  VL[illegible]CEA[illegible]KN  [illegible] 392
Db     1013 [illegible] [illegible] [illegible]VCAP[illegible] 1064

Qy     3[illegible] M[illegible] [illegible] 45[illegible]
Db     1065 [illegible]VF[illegible]DVDLNGS[illegible]SNIIFAPVLLFHSKIEESSC-  ----------  GSLHKL 1104

Qy     45[illegible] [illegible]KKRK[illegible]AKKK[illegible]KRSALFNSEEHSARYSNSNNSGSGASS---PLTSPSSPTPPSTS 508
Db     1[illegible] [illegible]KK[illegible]HDAL  NSKCAVKSP[illegible]PPA[illegible]PPPPKVK 1151

Qy     5[illegible] [illegible]PPAAPLPPASIEVPAQLSSQAVN 544
Db     1152 [illegible] 1194


RESULT      2
US-0[illegible]-2
; Sequence [illegible], Application US/[illegible]3930
; Patent No. [illegible]
; GENERAL INFORMATION:
;  APPLICANT: Dean, Nicholas M.
;  TITLE OF INVENTION: Antisense Oligonucleotide Modulation of Human Protein
;  TITLE OF INVENTION: Kinase C delta Expression
;  FILE REFERENCE: ISPH 0357
;  CURRENT APPLICATION NUMBER: US/[illegible]
;  CURRENT FILING DATE: 1999 05 18
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: [illegible]
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-[illegible]-2

  Query Match             4.8%;  Score 145;  DB 4;  Length 676;
  Best Local Similarity   2[illegible]%;  Pred. No. [illegible];
  Matches  [illegible];  Conservative   [illegible];  Mismatches  114;  Indels   84;  Gaps   15;

Qy     1[illegible] [illegible]KYLSDKDP[illegible] [illegible]YIYRVIFATANE[illegible] 234
Db     3[illegible] [illegible]KK[illegible]VV[illegible]IMVEKKVL  - [illegible]AAENF[illegible]FVML 428

Qy     235  K[illegible]YKAK[illegible] [illegible] 2[illegible]
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Qy     338 [illegible] [illegible] 384
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Db     650 NLIDSMDQ 657


RESULT      3
US-08-467-083-68
; Sequence 68, Application US/08467083
; Patent No. 5726023
;  GENERAL INFORMATION:
;     APPLICANT:  Cheever, Martin A.
;     APPLICANT:  Disis, Mary L.
;     TITLE OF INVENTION:  IMMUNE REACTIVITY TO HER-2/NEU PROTEIN
;     TITLE OF INVENTION:  FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
;     TITLE OF INVENTION:  HER-2/NEU ONCOGENE IS ASSOCIATED
;     NUMBER OF SEQUENCES:  68
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Seed and Berry
;       STREET:  6300 Columbia Center, 701 Fifth Avenue
;       CITY:  Seattle
;       STATE:  Washington
;       COUNTRY:  US
;       ZIP:  98104-7092
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/467,083
;       FILING DATE:  06-JUN-1995
;       CLASSIFICATION:  424
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/414,417
;       FILING DATE:  06-JUN-1995
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Sharkey, Richard G.
;       REGISTRATION NUMBER:  32,629
;       REFERENCE/DOCKET NUMBER:  [illegible]
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (206) 622-4900
;       TELEFAX:  (206) 682-6031
;       TELEX:  3723836 SEEDANBERRY
;   INFORMATION FOR SEQ ID NO:  68:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  1255 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
US-08-467-083-68

  Query Match             4.8%;  Score 144;  DB 1;  Length 1255;
  Best Local Similarity   19.4%;  Pred. No. 0.0029;
  Matches  121;  Conservative   77;  Mismatches  225;  Indels  200;  Gaps   26;

Qy     1[illegible] [illegible]AAI[illegible]AS[illegible] [illegible]VKRYC[illegible]NNSLQIAGLSLPLPPK 78
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Qy     79 KL[illegible]NMP[illegible]NVI[illegible]ANY[illegible]IALQQVS 137
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Qy    198 IKL[illegible]EEKYQNEKKI 257
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Qy    258 QQLELQQIKEYGRQ[illegible]HASNVML---------[illegible]RLLDLEN 308
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Qy    309 S    [illegible]MIYQ[illegible]EPPLSV 354
Db    875 IEYHADGGKVPIKWMALESILRRRF[illegible] 926

Qy    355 PVDSPP------PAPSMAVVAVLE[illegible]KNGMPLISRLLQMPLES 397
Db    927 PAREIPDLLEKGERLPQPPICTIDVYMIMVKCWMIDSECRPRFRELVSEFSRMARDPQRF 986

Qy    398 DVLLTTSEKPQPKIPTKLKEALRIAKEP---IEKRIEE[illegible]----KQIHQH 440
Db    987 VVIQNEDLGPASPLDSTFYRSLLEDDDMGDLVDAEEYLVPQQGFFCPDPAPGAGGMVHHR 1046

Qy    441 EELIEALHHH[illegible]EEEEEEIIAFEE[illegible]AS----- 493
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Qy    494              SPL    TSPSSPIPPSISE    ISALPEP--      -PPPPP 521
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Qy    522 PPAAPLPP-----ASTEVPAQLS 539
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RESULT 4
US-08-414-417B-68
; Sequence 68, Application US/08414417B
; Patent No. [illegible]
; GENERAL INFORMATION
; APPLICANT: [illegible]
; APPLICANT: Disis, Mary L.
; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
; TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
; TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/414,417B
; FILING DATE: 31-MAR-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharkey, Richard G.
; REGISTRATION NUMBER: 32,629
; REFERENCE/DOCKET NUMBER: [illegible] 448C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 68:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1255 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-414-417B-68

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  Query Match            4.8%;  Score 144;  DB [illegible];  Length 1255;
  Best Local Similarity  19.4%;  Pred. No. 0.0029;
  Matches 121;  Conservative  77;  Mismatches  227;  Indels  200;  Gaps  26;

Qy     19 ELTAATEAS[illegible]NNS[illegible]PPK 78
Db    650 FLISIISAVVGIL[illegible]LVVVLGVVFGIL[illegible]MRRLL[illegible]VEPLTPS 703

Qy     79 KLIGNMDKEPIAERQKGLQNYLNV[illegible]ANYIEIALQQVS 137
Db    704 GAMPNQ                    AQMRILKE[illegible]IVYKGIWI      740

Qy    138 M[illegible]EDEQS[illegible] 197
Db    741          [illegible]ENV         [illegible]                 [illegible]  772

Qy    198 [illegible]NEEKI 257
Db    773   VMAGVGSPYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGR       816

Qy    258 QQLELQQIKEYGRQ[illegible]HASNVM[illegible]PN 308
Db    817   LGSQDLLNWCMQIAKGMSYLEDVRLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDE 874

Qy    309 S              [illegible]BPPLSV 354
Db    875 IEYHADGGKVPIKWMALESILRRRF        [illegible] 926

Qy    355 PVDSPP---  -----PAPSMAVVAVLE[illegible]KNGMPLISRLLQMPLES 397
Db    927 PAREIPDLLEKGERLPQPPICTIDVYMIMVKCWMIDSECRPRFRELVSEFSRMARDPQRF 986

Qy    398 DVLLTTSEKPQPKIPTKLKEALRIAKEP---IEKRIEE---      --KQIHQH 440
Db    987 VVIQNEDLGPASPLDSTFYRSLLEDDDMGDLVDAEEYLVPQQGFFCPDPAPGAGGMVHHR 1046

Qy    441 EELIEA[illegible]AS -     493
Db   1047 HRSSSIRSGGG---------DLTLGLEPSEEEAPRSPLAPSEGAGSDVFDGDLG 1091

Qy    494              SPL    TSPSSPIPPSISE    ISALPEP -      -PPPPP 521
Db   1092 MGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYVNQPDVRPQPPS 1151

Qy    522 PPAAPLPP-----ASTEVPAQLS 539
Db   1152 PREGPLPAARPAGATLERPKTLS 1174
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RESULT 5
US-08-484-438-8
; Sequence 8, Application US/08484438
; Patent No. 5811098
; Patent No. 5811098 5780031
; GENERAL INFORMATION:
; APPLICANT: Plowman, Gregory D.
; APPLICANT: Culouscou, Jean Michel
; APPLICANT: Shoyab, Mohammed
; APPLICANT: Siegall, Clay B.
; APPLICANT: Hellstrom, Ingegerd
; APPLICANT: Hellstrom, Karl E.
; TITLE OF INVENTION: [illegible] KINASE

```
;    NUMBER OF SEQUENCES: 42
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE: Pennie & Edmonds
;      STREET: 1155 Avenue of the Americas
;      CITY: New York
;      STATE: New York
;      COUNTRY: U.S.A.
;      ZIP: 10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE: Floppy disk
;      COMPUTER: IBM PC compatible
;      OPERATING SYSTEM: PC-DOS/MS-DOS
;      SOFTWARE: PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER: US/08/461,142
;      FILING DATE: 07-JUN-1995
;      CLASSIFICATION: 530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER: 08/323,442
;      FILING DATE: 14-OCT-1994
;      APPLICATION NUMBER: US 08/150,704
;      FILING DATE: 10-NOV-1993
;      CLASSIFICATION: 530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER: US 07/981,165
;      FILING DATE: 24-NOV-1992
;      CLASSIFICATION: 540
;    ATTORNEY/AGENT INFORMATION:
;      NAME: Misrock, S. Leslie
;      REGISTRATION NUMBER: 18,872
;      REFERENCE/DOCKET NUMBER: 5621-230
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE: (212) 790-9090
;      TELEFAX: (212) 869-8864/9741
;      TELEX: 66141 PENNIE
;  INFORMATION FOR SEQ ID NO: 8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH: 1255 amino acids
;      TYPE: amino acid
;      STRANDEDNESS: unknown
;      TOPOLOGY: unknown
;    MOLECULE TYPE: protein
US-08-461-142-8

  Query Match             4.8%;  Score 144;  DB 2;  Length 1255;
  Best Local Similarity   19.1%;  Pred. No. 0.0029;
  Matches  121;  Conservative   80;  Mismatches  230;  Indels  198;  Gaps   26;

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Qy      198 [illegible]YTYRV[illegible]AIANG[illegible]YKAKPK[illegible]KKY[illegible]NPKKI 257
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Db      817   [illegible]LNWCMQIAKGMSYLEDVRLVHRDLAARNVLVKSPNHVKI[illegible]CLARLLDIDE 874

Qy      [illegible]            [illegible]PSFYRSYF[illegible]LVH[illegible] 354
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Qy      398 DVLLTTSEKPQSKPGTSGKEAAGKKAKPC       GKRLTEEQ-        KLHQH 440
Db      987 VVIQNEDLGPASPLDSTFYRSLLEDDDMGDLVDAEEYLVPQQGFFCPDPAPGAGGMVHHR 1046

Qy      441 [illegible]                                          493
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Qy      522 PPAAPLPPASTEVPAQLSSQAVNGMSRG 549
Db     1152 PREGPLPAAR---PAGATLERAKTLSPG 1176

RESULT 6
US-08-486-348A-68
; Sequence 68, Application US/08486348A
; Patent No. 5846538
;  GENERAL INFORMATION:
;    APPLICANT: Cheever, Martin A.
;    APPLICANT: Disis, Mary L.
;    TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
;    TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
;    TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED
;    NUMBER OF SEQUENCES: 69
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE: Seed and Berry LLP
;      STREET: 6300 Columbia Center, 701 Fifth Avenue
;      CITY: Seattle
;      STATE: Washington
;      COUNTRY: US
;      ZIP: 98104-7092
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE: Floppy disk
;      COMPUTER: IBM PC compatible
;      OPERATING SYSTEM: PC-DOS/MS-DOS
;      SOFTWARE: PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER: US/08/486,348A
;      FILING DATE: 07-JUN-1995
;      CLASSIFICATION: 424
;    ATTORNEY/AGENT INFORMATION:
;      NAME: Sharkey, Richard G.
;      REGISTRATION NUMBER: 32,629
;      REFERENCE/DOCKET NUMBER: 920010.448C6
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE: (206) 622-4900
;      TELEFAX: (206) 682-6031
;  INFORMATION FOR SEQ ID NO: 68:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH: 1255 amino acids
;      TYPE: amino acid
;      TOPOLOGY: linear
US-08-486-348A-68

  Query Match             4.8%;  Score 144;  DB 2;  Length 1255;
  Best Local Similarity   19.4%;  Pred. No. 0.0029;
  Matches  121;  Conservative   77;  Mismatches  227;  Indels  200;  Gaps   26;

Qy       19 PLTAATEASQSTQSHTEYTTPVQRGTSVENSWQIVRRYSDFDLLNNSLQIAGLSLPLPPK 78
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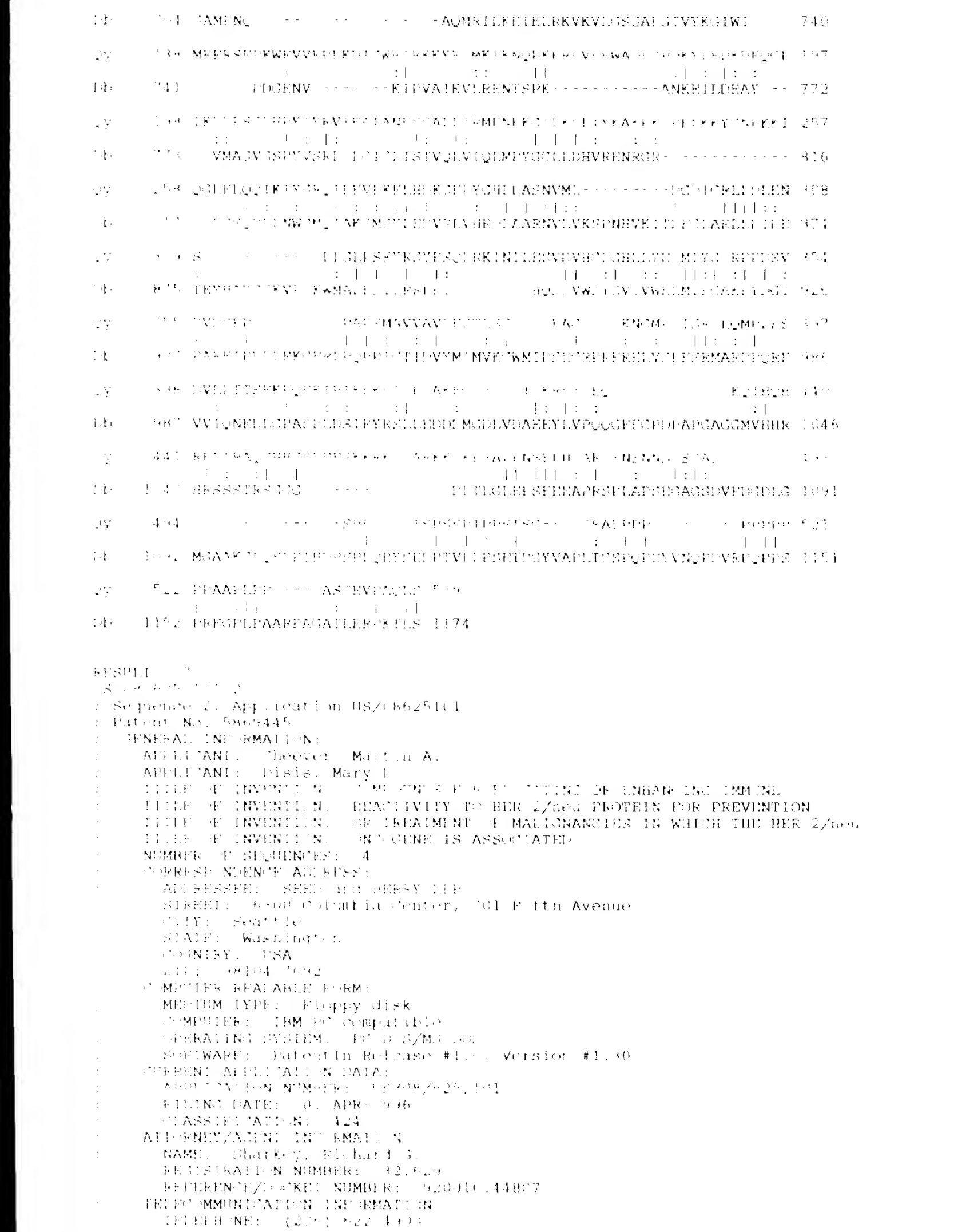

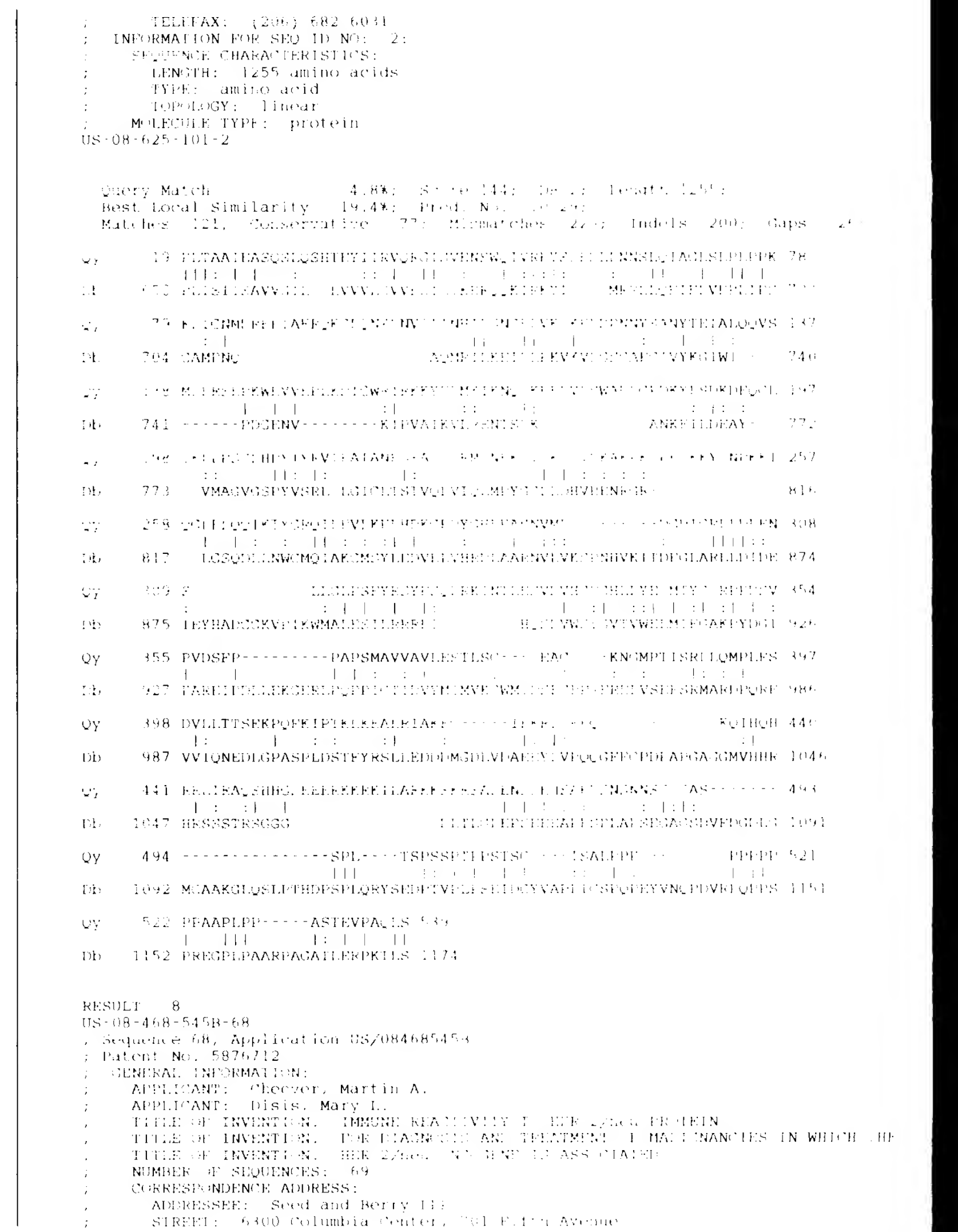

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;       CITY:  Seattle
;       STATE:  Washington
;       COUNTRY:  US
;       ZIP:  98104-7092
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/468,545B
;       FILING DATE:  06-JUN-1995
;       CLASSIFICATION:  424
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Sharkey, Richard G.
;       REGISTRATION NUMBER:  32,629
;       REFERENCE/DOCKET NUMBER:  920010.448C5
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (206) 622-4900
;       TELEFAX:  (206) 682-6031
;   INFORMATION FOR SEQ ID NO:  68:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  1255 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
US-08-468-545B-68

  Query Match             4.8%;  Score 144;  DB 2;  Length 1255;
  Best Local Similarity   19.4%;  Pred. No. 0.0029;
  Matches  121;  Conservative   77;  Mismatches  225;  Indels  200;  Gaps   26;

Qy         19 PLTAAIEASQSLQSHTEYIIRVQRGISVENSWQIVRRYSDFDLLNNSLQIAGLSLPLPPK 78
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Qy         79 KLIGNMDREFIAERQKGLQNYLNVIINHILSNCELVK KFLDPNNYSANYTEIALQQVS 137
Db        704 GAMPNQ                      AQMRILKETELRKVKVLGSGAFGTVYKGIWI    740

Qy        138 MFFRSEPKWEVVEPLKDIGWRIRKKYFLMKIKNQPKERLVLSWADEGPDKYLSQKDFQCL 197
Db        741       PDGENV          KIPVAIKVLRENISPK                ANKEILDEAY    772

Qy        198 IKLLPSCLHPYIYRVIFATANESSALLIRMFNEKGTLKDLIYKAKPKDPFLKKYCNPKKI 257
Db        773   VMAGVGSPYVSRL LGICLTSTVQLVTQLMPYGCLLDHVRENRGR   --     - ---- 816

Qy        258 QGLELQQIKIYGRQILEVLKFLHDKGFPYGHLHASNVML --     --- DGDTCRLLDLEN 308
Db        817   LGSQDLLNWCMQIAKGMSYLEDVRLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDE 874

Qy        309 [illegible]          LLGLPSFYRSYFSQFRKINFLESVDVHCFGHLLYE MIYG RPPDSV 354
Db        875 TEYHADGGKVPIKWMALESILRRRFT            HQSDVWSYGVTVWELMTFGAKPYDGI 926

Qy        355 PVDGFP            FAPSMAVVAVLESILSC      EAC  --  KNGMPTSRLLQMPLFS 397
Db        927 PAREIPDLLEKGERLPQPPICTIDVYMIMVKCWMIDSECRPRFRELVSEFSRMARDPQRF 986

Qy        398 IVILTISEKPQEKIPIFLKKALRIAKE      IEKRLIEEQ-------  ---  KQIHQE 449
Db        987 VVIQNEDLGPASPLDSTFYRSLLEDDDMGDLVDAEEYLVPQQGFFCPDPAPGAGGMVHHR 1046

Qy        441 FFLIRAQSHHGSEEERKKKKILARKKSKRSALENSEEHSARYSNSNNSGSGAS------- 493
Db       1047 HRSSSTRSGGG                  DLTLGLEPSEEEAPRSPLAPSEGAGSDVFDGDLG 1091

Qy        494               SPL     ISPSSPIPPSISG-     ISALPPP-    -      PPPPP 521
Db       1092 MGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYVNQPDVRPQPPS 1151

Qy        522 PPAAPLPP      ASIEVPAQLS 539
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RESULT 9
US-08-356-786-2
; Sequence 2, Application US/08356786
; Patent No. 5877305
;  GENERAL INFORMATION:
;    APPLICANT:  Huston, James S.
;    APPLICANT:  Oppermann, Hermann
;    APPLICANT:  Houston, L. L.
;    APPLICANT:  Ring, David B.
;    TITLE OF INVENTION:  Biosynthetic Binding Protein for Cancer
;    TITLE OF INVENTION:  Marker
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Edmund R. Pitcher, Testa, Hurwitz, & Thibeault
;      STREET:  Exchange Place, 53 State Street
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/356,786
;      FILING DATE:
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/831,967
;      FILING DATE:  06-FEB-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Pitcher, Edmund R.
;      REGISTRATION NUMBER:  27,829
;      REFERENCE/DOCKET NUMBER:  CRP-053
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 248-7000
;      TELEFAX:  (617) 248-7100
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1255 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-356-786-2

  Query Match             4.8%;  Score 144;  DB 2;  Length 1255;
  Best Local Similarity   19.4%;  Pred. No. 0.0029;
  Matches  121;  Conservative   77;  Mismatches  225;  Indels  200;  Gaps   26;

Qy         19 PLTAAIEASQSLQSHTEYIIRVQRGISVENSWQIVRRYSDFDLLNNSLQIAGLSLPLPPK 78
Db        650 PLTSIISAVVGIL--LVVVLGVVFGILIKRRQQKIRKYI--MRRLLQETELVEPLTPS 703

Qy         79 KLIGNMDREFIAERQKGLQNYLNVIINHILSNCELVK KFLDPNNYSANYTEIALQQVS 137
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Qy        138 MFFRSEPKWEVVEPLKDIGWRIRKKYFLMKIKNQPKERLVLSWADEGPDKYLSQKDFQCL 197
Db        741 ------PDGENV--------KIPVAIKVLRENISPK    -  ---ANKEILDEAY--- 772

Qy        198 IKLLPSCLHPYIYRVIFATANESSALLIRMFNEKGTLKDLIYKAKPKDPFLKKYCNPKKI 257
Db        773 --VMAGVGSPYVSRL-LGICLTSTVQLVTQLMPYGCLLDHVRENRGR--    -      816

Qy        258 QGLELQQIKIYGRQILEVLKFLHDKGFPYGHLHASNVML            DGDTCRLLDLEN 308
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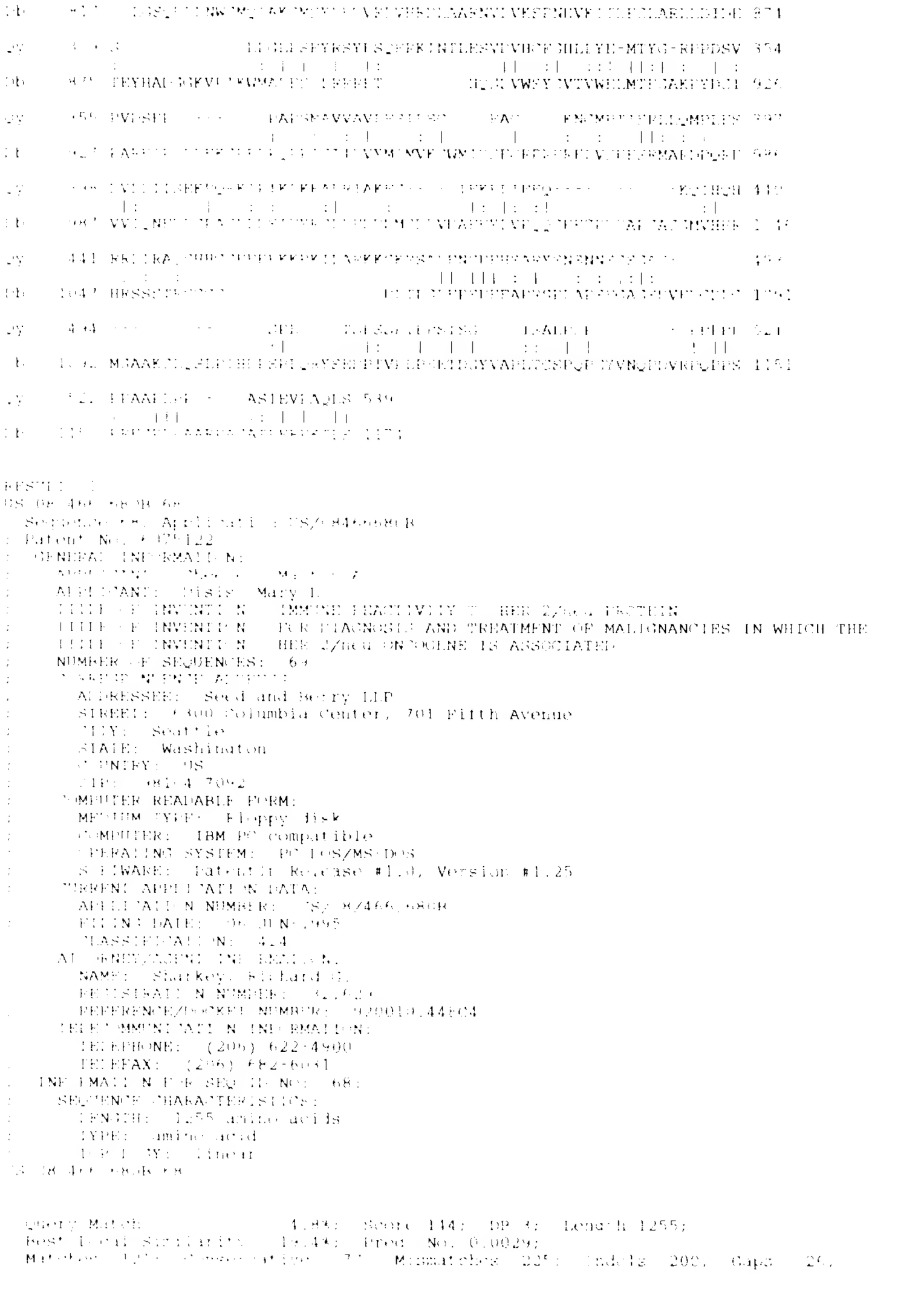

RESULT 10
US-09-684-458-2
; Sequence 2, Application US/09684458
; Patent No. 6080838
; GENERAL INFORMATION:
; APPLICANT: Dietz, Mary L.
; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER 2/neu PROTEIN
; TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
; TITLE OF INVENTION: HER 2/neu ONCOGENE IS ASSOCIATED
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/466,080B
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Starkey, Richard G.
; REGISTRATION NUMBER: 32,629
; REFERENCE/DOCKET NUMBER: 960010.444C4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 68:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1255 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

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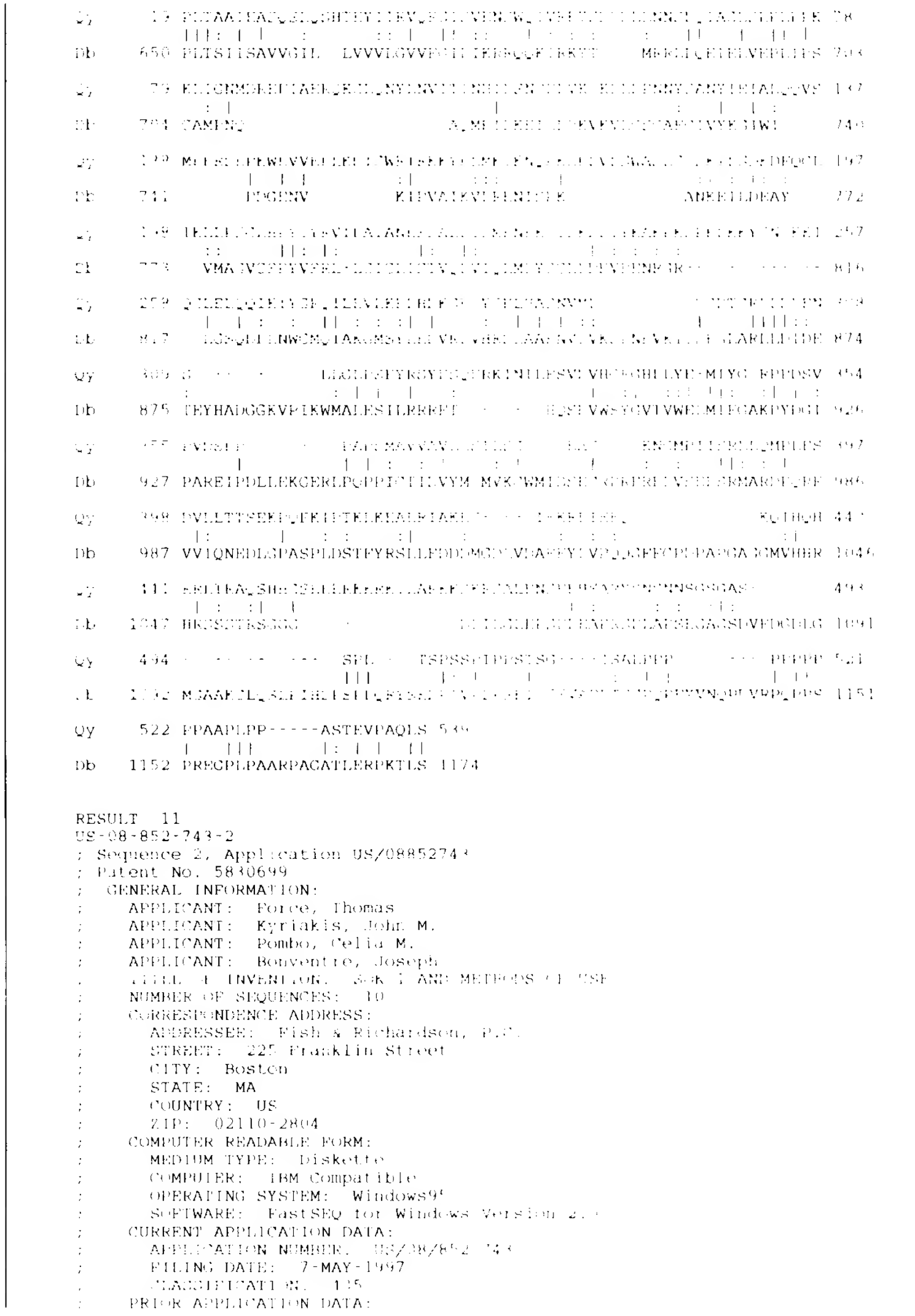

RESULT 11
US-08-852-743-2
; Sequence 2, Application US/08852743
; Patent No. 5830699
; GENERAL INFORMATION:
; APPLICANT: Force, Thomas
; APPLICANT: Kyriakis, John M.
; APPLICANT: Pombo, Celia M.
; APPLICANT: Bonventre, Joseph
; TITLE OF INVENTION: SAK 1 AND METHODS OF USE
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/852,743
; FILING DATE: 7-MAY-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:

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      APPLICATION NUMBER: 60/016,774
      FILING DATE: [illegible] MAY 1996
    ATTORNEY/AGENT INFORMATION:
      NAME: Fraser, Janis K.
      REGISTRATION NUMBER: 34,819
      REFERENCE/DOCKET NUMBER: 07780/022001
    TELECOMMUNICATION INFORMATION:
      TELEPHONE: 617/542-5070
      TELEFAX: 617/542-[illegible]
      TELEX: 200154
  INFORMATION FOR SEQ ID NO: 2:
    SEQUENCE CHARACTERISTICS:
      LENGTH: 426 amino acids
      TYPE: amino acid
      TOPOLOGY: linear
    MOLECULE TYPE: protein
    FRAGMENT TYPE: internal
US-08-852-743-2

  Query Match             4.7%;  Score 142;  DB 2;  Length 426;
  Best Local Similarity   23.6%;  Pred. No. 0.00092;
  Matches   98;  Conservative   56;  Mismatches  163;  Indels   98;  Gaps   20;

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Qy    226 EMENEKQILKDLIYKAKPKDPT[illegible]LHEKGFP 285

Db     95 MEYLGGGSALDLL---KP---------GP------LEEIYIATILREILKGLDYLHSEKKI 137

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Db    281 TELIDRYK-----RWKSEGHGEESSSEDS---DIDGEAEDGEQGPIWI------------ 320

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RESULT 12
US-09-211-930-4
; Sequence 4, Application US/09211930
; Patent No. 5962265
; GENERAL INFORMATION:
;  APPLICANT: Tyrell E. No. 5962265ris
;  APPLICANT: William Craig Moore
;  APPLICANT: David Chay Silberstein
;  TITLE OF INVENTION: HUMAN SIGNAL TRANSDUCTION
;  TITLE OF INVENTION: SERINE/THREONINE KINASE
;  FILE REFERENCE: PHM 70296
;  CURRENT APPLICATION NUMBER: US/09/211,930
;  CURRENT FILING DATE: 1998-12-15
;  EARLIER APPLICATION NUMBER: GB 9726851.0
;  EARLIER FILING DATE: 1997-12-19
;  NUMBER OF SEQ ID NOS: 14
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 4
;   LENGTH: 426
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-211-930-4

  Query Match             4.7%;  Score 142;  DB 2;  Length 426;
  Best Local Similarity   23.6%;  Pred. No. 0.00092;
  Matches   98;  Conservative   56;  Mismatches  163;  Indels   98;  Gaps   20;

Qy    168 IKNQPKERIVISWAPI---QPDKYLSPKDFQ[illegible]LIKELLPSQHPY[illegible]YRVIFATANESSALLI 225

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Qy    226 EMENEKQILKDLIYKAKPKDPT[illegible]LHEKGFP 285

Db     95 MEYLGGGSALDLL---KP---------GP------LEEIYIATILREILKGLDYLHSEKKI 137

Qy    286 YGHLHASNVML--DGDICRLLDL---------------ENSLLGLPSFYRSYFSQFRKINILE 331

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Db    194 FKADIWSLGITAIELAKGEPPNS---DLHP-----MRVLFLIP-----------KNSPPTLEGQ 238

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Qy    451 QSIEEEKKPKIIAPKKSKP[illegible]AIEN[illegible]EEHEAPYSNCNNP[illegible]QASSPLLSPESQPTPP[illegible]GQI 510

Db    281 TELIDRYK-----RWKSEGHGEESSSEDS---DIDGEAEDGEQGPIWI------------ 320

Qy    511 SALPPPPPPPPPAAPLPPASTEVPAQLQQAVNGMQRGALLQSIQNPLEGILEK 565

Db    321 ----EPPTIRPSPHSKLHKGTALHSSQKPADAVKRQPRSQ[illegible]LSILVRPVPGELKE 371

RESULT 13
US-09-340-993-4
; Sequence 4, Application US/09340993
; Patent No. 6034228
; GENERAL INFORMATION:
;  APPLICANT: Tyrell E. No. 6034228ris
;  APPLICANT: William Craig Moore
;  APPLICANT: David Chay Silberstein
;  TITLE OF INVENTION: HUMAN SIGNAL TRANSDUCTION SERINE/THREONINE KINASE
;  FILE REFERENCE: PHM.70296.N1
;  CURRENT APPLICATION NUMBER: US/09/340,993
;  CURRENT FILING DATE: 1999-06-25
;  EARLIER APPLICATION NUMBER: GB 9726851.0 & US 09/211,930
;  EARLIER FILING DATE: 1997-12-19 & 1998-12-15
;  NUMBER OF SEQ ID NOS: 14
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 4
;   LENGTH: 426
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-340-993-4

  Query Match             4.7%;  Score 142;  DB 3;  Length 426;
  Best Local Similarity   23.6%;  Pred. No. 0.00092;
  Matches   98;  Conservative   56;  Mismatches  163;  Indels   98;  Gaps   20;

Qy    168 IKNQPKERIVISWAPI---QPDKYLSPKDFQ[illegible]LIKELLPSQHPY[illegible]YRVIFATANESSALLI 225

Db     38 IDNHTKEVVAIKIIDLEEAEDEI---EDIQQEIIVLSQCDSPYIIRYFGSYLKSTKLWII 94

Qy    226 EMENEKQILKDLIYKAKPKDPT[illegible]LHEKGFP 285

Db     95 MEYLGGGSALDLL---KP---------GP------LEEIYIATILREILKGLDYLHSEKKI 137

Qy    286 YGHLHASNVML--DGDICRLLDL---------------ENSLLGLPSFYRSYFSQFRKINILE 331
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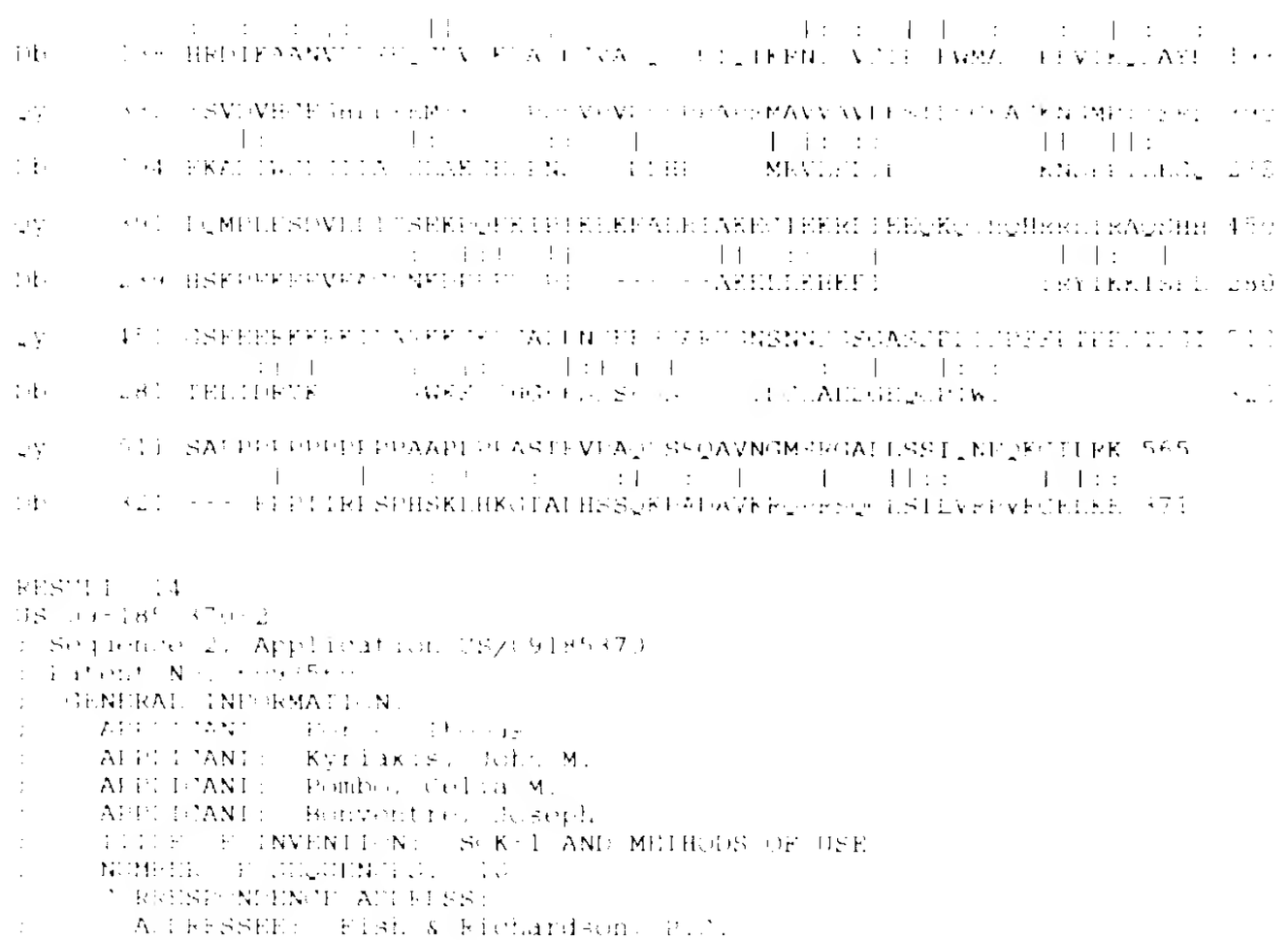

RESULT 14
US-09-185-370-2
; Sequence 2, Application US/09185370
; Patent No. 6265537
; GENERAL INFORMATION:
; APPLICANT: Kyriakis, John M.
; APPLICANT: Pombo, Celia M.
; APPLICANT: Bonventre, Joseph.
; TITLE OF INVENTION: SCK-1 AND METHODS OF USE
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3½ Disk
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/185,370
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/852,274
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 00786/327001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 426 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-09-185-370-2

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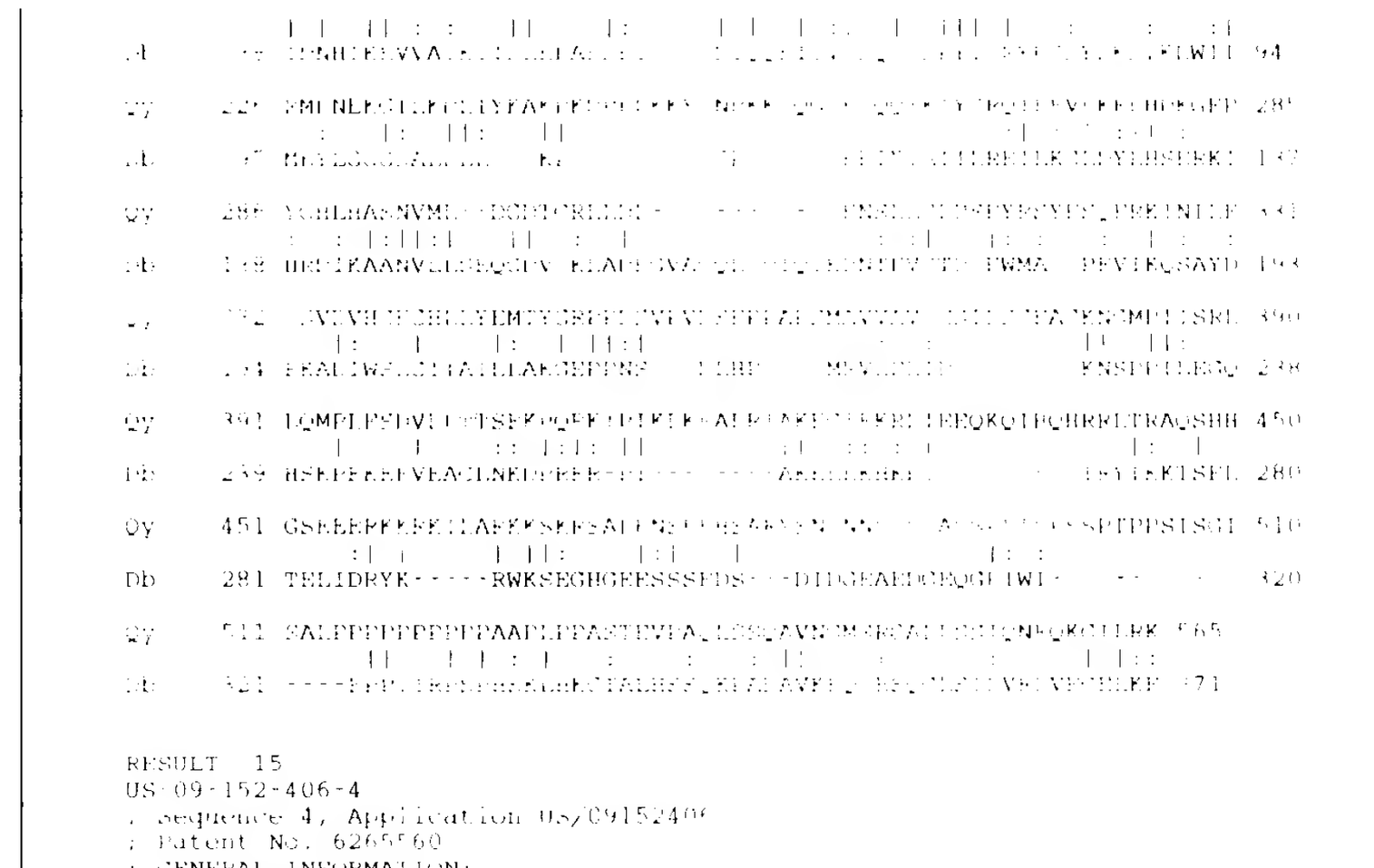
Matches 98; Conservative 56; Mismatches 163; Indels 98; Gaps 20;



RESULT 15
US-09-152-406-4
; Sequence 4, Application US/09152406
; Patent No. 6265560
; GENERAL INFORMATION:
; APPLICANT: William Craig Moore
; APPLICANT: Tyrell E. No. 6265560rris
; APPLICANT: David Shay Silberstein
; TITLE OF INVENTION: HUMAN STE20 LIKE SERINE ACTIVATED
; TITLE OF INVENTION: SERINE/THREONINE KINASE
; FILE REFERENCE: PHM.70272
; PRESENT APPLICATION NUMBER: US/09/152,406
; CURRENT FILING DATE: 1998-09-14
; EARLIER APPLICATION NUMBER: 971992.2
; EARLIER FILING DATE: 1997-09-19
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 426
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-152-406-4

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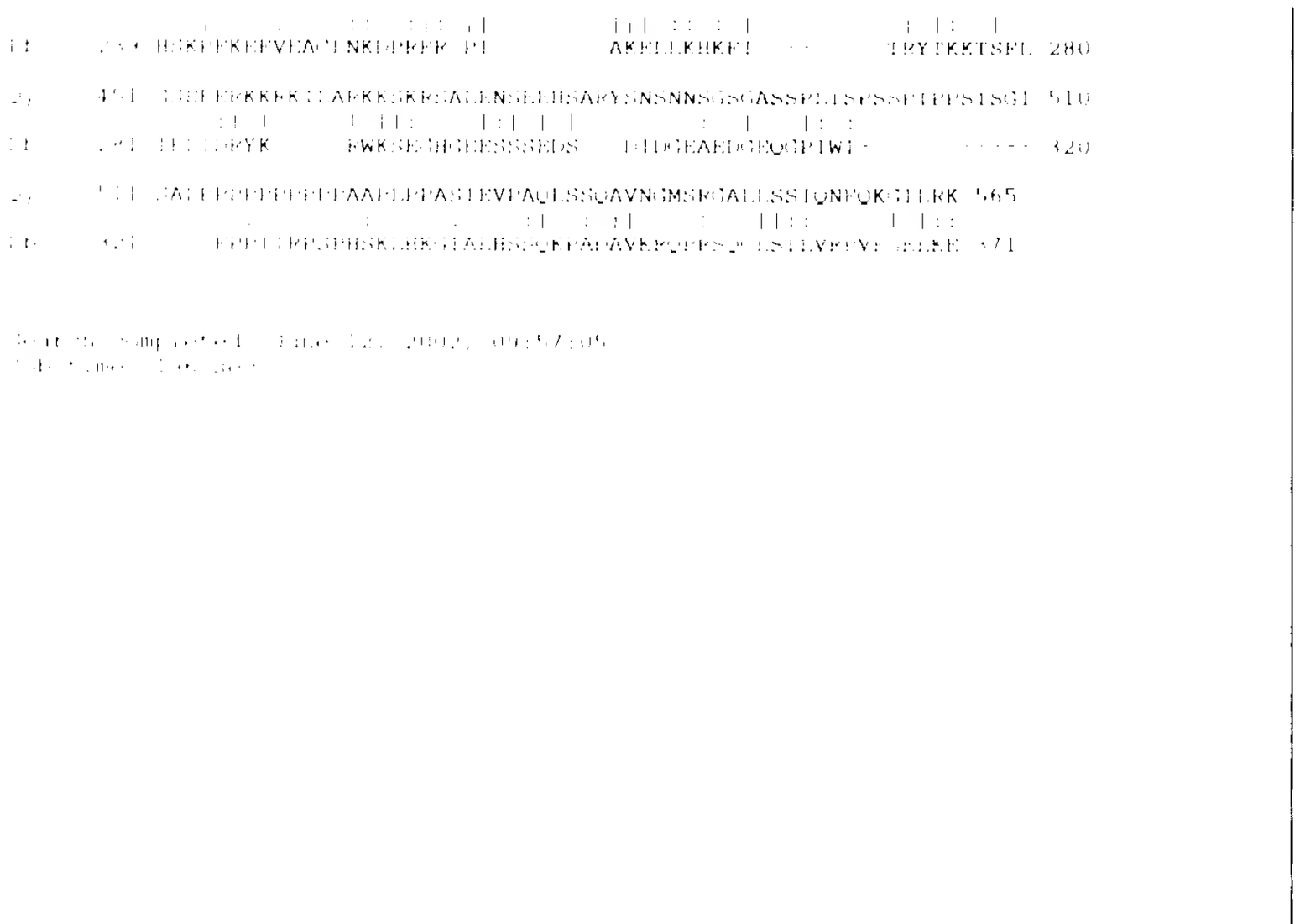

SeqSearch version 4.5
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SW protein protein search, using sw model

Run on: June 12, 2002, 09:55:52 ; Search time 707.44 Seconds
(without alignments)
529.059 Million cell updates/sec

Title: US-09-684-458-2
Perfect score: 3245
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 179049299 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: SPTREMBL_14:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_rest:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
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2	2791.5	86.1	582	11	Q91wb6	Q91wb6 mus musculu
3	2825.5	87.1	515	4	Q96R07	Q96r07 homo sapien
4	2753	78.3	450	4	Q96CA3	Q96ca3 homo sapien
5	2687.5	24.3	459	5	Q95RK3	Q95rk3 drosophila
6	973	30.1	565	5	Q9V844	Q9v844 drosophila
7	1662.5	18.1	515	5	Q61564	Q61564 drosophila
8	1662.5	18.1	515	5	Q9VLZ4	Q9vlz4 drosophila
9	957	11.9	280	5	Q95SL3	Q95sl3 drosophila
10	211.5	7.0	496	4	Q96BF1	Q96bf1 homo sapien
11	234.5	6.8	459	11	Q9EEE3	Q9eee3 mus musculu
12	182	5.1	1851	5	Q18657	Q18657 caenorhabdi
13	179	5.9	1112	4	Q96PY5	Q96py5 homo sapien
14	174	5.7	1231	4	Q96DT8	Q96dt8 homo sapien
15	172	5.7	1245	4	Q96J92	Q96j92 homo sapien
16	172	5.7	2126	11	Q9JIH7	Q9jih7 rattus norv
17	171.5	5.7	670	4	Q9P [illegible]	Q9p1s9 homo sapien
18	171.5	5.7	1228	5	[illegible]	Q17566 caenorhabd
19	171.5	5.7	2382	4	Q9H3A5	Q9h3a5 homo sapien
20	166	5.5	513	13	Q9[illegible]P2	Q9dez2 gallus gal
21	164.5	5.5	1043	5	Q8V[illegible]	Q8vuc6 drosophila
22	163	5.4	1504	4	Q96[illegible]	Q96ues6 homo sapien
23	163	5.4	1528	4	Q9Y[illegible]	Q9y2i1 homo sapien
24	162.5	5.4	407	5	Q9V[illegible]	Q9v8c9 drosophila
25	161.5	5.4	344	11	Q9[illegible]	Q9d[illegible] mus musculus
26	161.5	5.4	1062	5	Q95[illegible]	Q95qp7 caenorhabd
27	159	5.3	779	4	Q9B[illegible]	Q9b1p4 homo sapien
28	158.5	5.3	550	13	Q9[illegible]	Q9z2c3 gallus gal
29	158.5	5.3	1032	16	Q9[illegible]	Q9c1f58 pseudomonas
30	158	5.3	901	10	Q9[illegible]	Q9s8h7 oryza sativ
31	158	5.3	1206	11	[illegible]	[illegible]8815 rattus norv
32	158	5.3	1231	11	[illegible]	[illegible]0w2 cavia porce
33	157.5	5.2	1189	5	Q9Y11[illegible]	Q9y111 drosophila
34	157.5	5.2	1189	5	Q9W[illegible]	Q9w378 drosophila
35	156	5.2	429	4	Q9H[illegible]	Q9nkq5 homo sapien
36	156	5.2	558	10	Q9M8S2	Q9m8s2 arabidopsis
37	155.5	5.2	1202	11	Q9WU[illegible]	Q9wu41 mus musculu
38	155.5	5.2	1233	11	[illegible]54988	[illegible]54988 mus musculu
39	155.5	5.2	1450	4	Q9BYP7	Q9byp7 homo sapien
40	154.5	5.1	907	10	Q9[illegible]46	Q9e946 arabidopsis
41	153.5	5.1	643	2	Q9S478	Q9s478 myxococcus
42	153.5	5.1	884	4	Q9Y[illegible]5	Q9y6r5 homo sapien
43	153.5	5.1	1621	5	[illegible]01900	[illegible]01900 caenorhabd
44	153	5.1	576	2	Q9XA04	Q9xa04 streptomyce
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ALIGNMENTS

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AC Q9NXB8;
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DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE CDNA FLJ20335 FIS, CLONE HEP14.9 (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kawakami T., Nagaoki S., Itoh T., Shiba K., Sonta T., Matsumura K.,
RA Nakajima Y., Mizuno T., Morinaga M., Ota T., Suzuki T., Obayashi M.,
RA Nishi T., Shibahara T., Tanaka T., Nakamura Y., Isogai T., Sugano S.;
RT "NEDO human cDNA sequencing project.";
RL Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AK000342; BAA91097.1; -.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR001683; PX.
DR InterPro; IPR003124; WH2.
DR Pfam; PF00069; WH2; 1.
DR SMART; SM00312; PX; 1.
DR SMART; SM00246; WH2; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW ATP binding; Transferase.
FT NON_TER 649 649
SQ SEQUENCE 649 AA; 73006 MW; [illegible] CRC64;

Query Match 97.3%; Score 2919.5; DB 4; Length 649;
Best Local Similarity 96.3%; Pred. No. 2.8e-259;
Matches 567; Conservative 9; Mismatches 8; Indels 13; Gaps 2;

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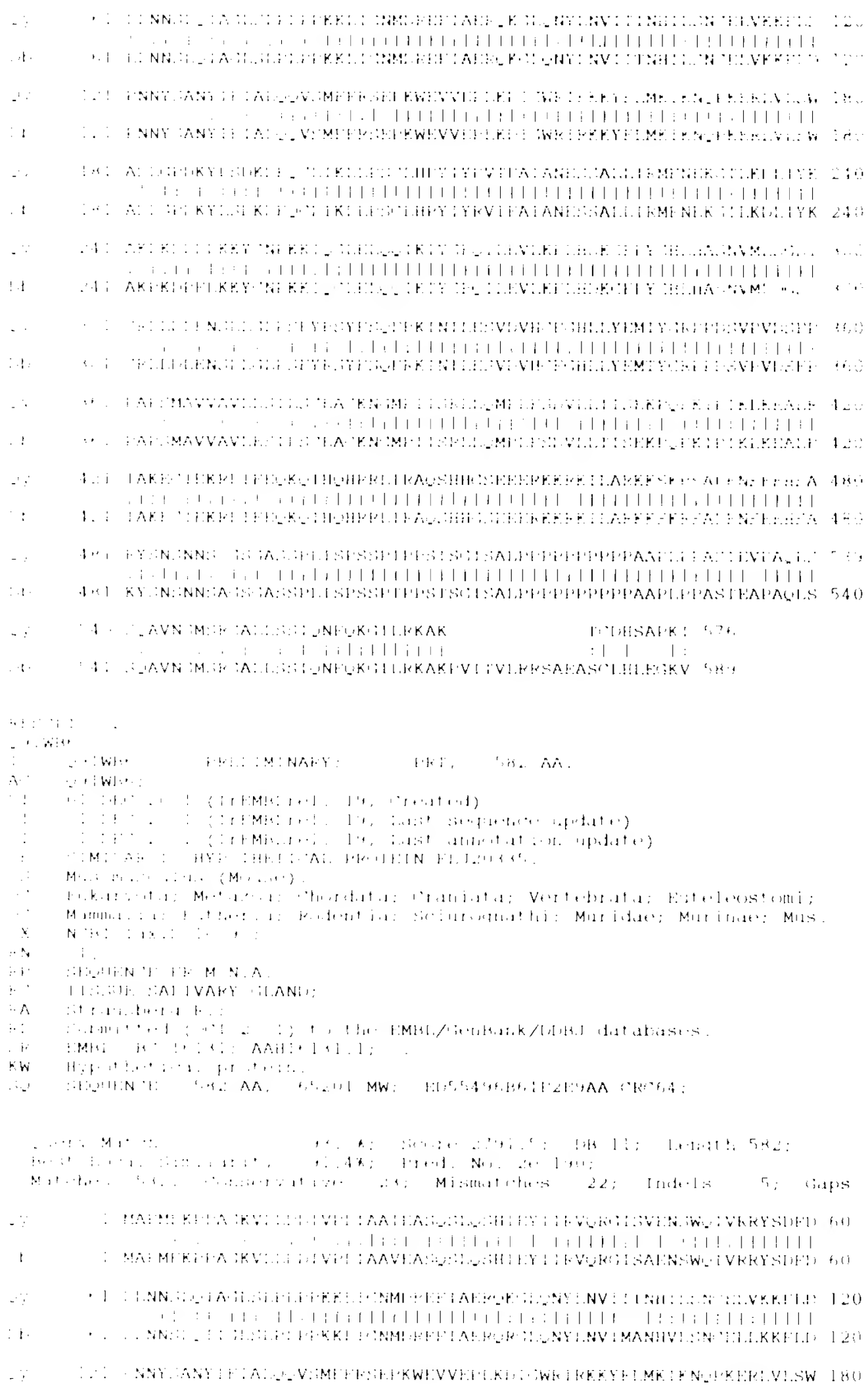

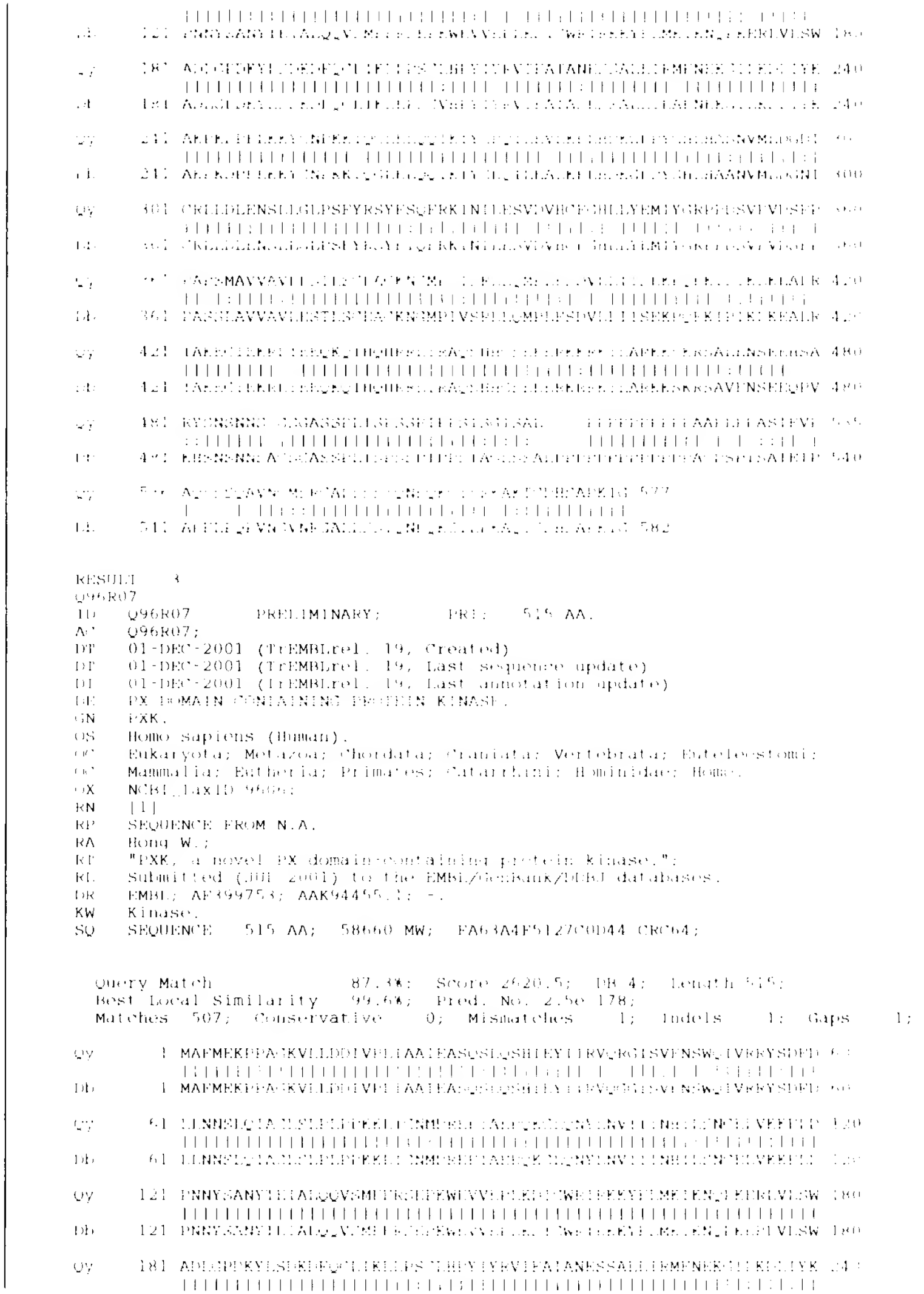

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AC Q96R07;
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DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE PX DOMAIN CONTAINING PROTEIN KINASE.
GN PXK.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Hong W.;
RT "PXK, a novel PX domain-containing protein kinase.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF399753; AAK94455.1; -.
KW Kinase.
SQ SEQUENCE 515 AA; 58660 MW; FA63A4F5127C0D44 CRC64;

Query Match 87.4%; Score 2620.5; DB 4; Length 515;
Best Local Similarity 99.6%; Pred. No. 2.5e-178;
Matches 507; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

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Qy      301 [illegible] 360
Db      301 [illegible]KINTLESVDVH[illegible]FGHLLYEMIYGRPPDSVPVDSFP 360

Qy      361 FAPSMAVVAVLESILSCEACKNGMPTISKLLQMPLFSDVLLTTSEKPQFKIPTKLKEALR 420
Db      361 FAPSMAVVAVLESILSCEACKNGMPTISKLLQMPLFSDVLLTTSEKPQFKIPTKLKEALR 420

Qy      421 IAK[illegible]ALENSLHSA 480
Db      421 IAK[illegible]ALENS[illegible]HA 480

Qy      481 RYSNGNNS[illegible]SSPTEPSTS 508
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DT   [illegible] (TrEMBLrel. 1[illegible], Created)
DT   [illegible] (TrEMBLrel. 1[illegible], Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   HYPOTHETICAL [illegible] KDA PROTEIN.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID [illegible]
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=PRIMARY B-CELLS FROM TONSILS;
RA   Strausberg R.;
RL   Submitted (SEP-2[illegible]) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC[illegible]; AAH1447[illegible].
KW   Hypothetical protein.
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Db       61 [illegible]NVIIENH[illegible]ELVKKFLD 120

Qy      121 PNNY[illegible]EWEVVEELK[illegible]KERLVLSW 180
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Qy      241 AK[illegible]KKY[illegible]NPKK[illegible]VLKPLHDKGFFY[illegible]ELHASNVMLDGDT 300
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Db      301 [illegible]SVDVH[illegible]GHLLYEMTYGRPPDSVPVDSFP 360
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Db      361 FAPSMAVVAVLE[illegible]KLKEALR 420

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AC   Q95RK3;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   [illegible]
GN   CG8726.
OS   Drosophila melanogaster (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC   Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID 7227;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN Y; CN BW SP;
RA   Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA   Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
RA   Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
RA   Nunoo J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K.,
RA   Yu C., Lewis S.E., Rubin G.M., Celniker S.;
RL   Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY061314; AAL28862.1; -.
SQ   SEQUENCE   450 AA;  50748 MW;  [illegible] CRC64;

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  Best Local Similarity   40.2%;  Pred. No. 1.[illegible]e-54;
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Qy       71 LSLPLPPKKL[illegible]NM[illegible]TAE[illegible]NNY[illegible]ANYIE 130
Db       71 IELPLPRKK[illegible]GNM[illegible]IAE[illegible]YI[illegible]AKKPV[illegible]PHD 130

Qy      131 IALQQVSMFFRSEPKWEVVEELK[illegible]KER 175
Db      131 HAVQNAM[illegible]LENDTTWS[illegible]VESGSQIHQ 188

Qy      176 -------------------------[illegible]LVLSWADLGPLKY[illegible]SDKDFQCL[illegible]KLLFSCLHPYI 209
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Db      249 EPVLLAAHTENGCLVIRKPHKIGTLK[illegible]NPEGPTALSMKQVATY 308

Qy      269 [illegible]QILEVLKPLHDKGFFYGHLHASNVM[illegible]FFKIN 328
Db      309 GKQILEALIFLHSKGYAYGHLHSGN[illegible]GVPAFYEPFEMQHSKIH 368

Qy      329 TLESVDVHCFGHLLYEMTYGRPPDSVPVDSFPFAPSMAVVAVLESILSCEACKNGMPTIS 388
Db      369 AIETIDVYCFGHVLFEMAMGYPLQESVVRQ[illegible]ESILSKEACKAGLPILF 427

Qy      389 RLLQMPLFSDVLLTTSEK 406
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DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   CG8726 PROTEIN.
GN   CG8726.
OS   Drosophila melanogaster (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC   Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7227;
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RP   SEQUENCE FROM N.A.
RC   STRAIN=BERKELEY;
RX   MEDLINE=20196006; PubMed=10731132;
RA   Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA   Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA   George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA   Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA   Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA   Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA   Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA   Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA   Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA   Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA   Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA   Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA   de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA   Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA   Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA   Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA   Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA   Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA   Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA   Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA   Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA   Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA   Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA   Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA   Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA   Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA   Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA   Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA   Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA   Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
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RA   Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA   Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA   Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA   Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA   Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT   "The genome sequence of Drosophila melanogaster.";
RL   Science 287:2185-2195(2000).
DR   EMBL; AE003563; AAF59158.1; -.
DR   FlyBase; FBgn0033244; CG8726.
DR   InterPro; IPR000719; Euk_pkinase.
DR   Pfam; PF00069; pkinase; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW   ATP-binding; Transferase.
SQ   SEQUENCE   563 AA;  62623 MW;  2517DC20C6671AEF CRC64;

  Query Match             29.1%;  Score 874;  DB 5;  Length 563;
  Best Local Similarity   30.2%;  Pred. No. 4.4e-54;
  Matches  173;  Conservative   90;  Mismatches  188;  Indels   64;  Gaps   11;

Qy         84 MDRREFIAKRQKHGQNYENVIIINHIIGNCIIVKEFIIENNYSANTIIIAIQQVLMEIKIL 143
Db          1 MEIEHFIAKRKLALGYINAVIMKRIIAGILAKRFVIIIYTQQQFHQHAVQNAMEIKN 

Qy        144 PEWLVVIFLFIIGWRIFKKIIIMRIENQFEER----                      175
Db         61 LIWSLGGSMGAIGWRLRKHYF--EVIIKFPTKSSNKQLVKSCSQIHQSKHFAAGSSNGSG 118

Qy        176                 LVLGWAIIDPLKYLSIKIIQLLKIIPTLHPYIYKVIFAIANIIIA 222
Db        119 HSIDACTLDPGSEVVAEWLEYGPDKFIDEKKIGGIMKSLMGLQHPHIEPVLLAAHTENGC 178

Qy        223 IIEEMFNEFTLEKIIYEAKIKIIFLEEYNIKKIQIIIIIQIEIYIKQIIIVIKIIGH 281
Db        179 LVIKRKNNIILKMVLMAAMKMLIIIKKINKKIIAIIMKQNAIIKQIIAIIIIAK 238

Qy        282 KGFPYGHLHASNVMLPGDTCRLLDLENSLIGEPSFYRSYFSQFRKINILESVDVHCPGHI 341
Db        239 KGYAYGHLHSGNIVIVDDTVKLLDIENPLLIVPAIYRPFIRQHGKIHAIIIIVYCPGHV 298

Qy        342 LYEMITGRFFLQVEVIGFPIAEFMAVVAVLIIIILIIHATKNGMPIISRLLQMPLFSDVLI 401
Db        299 LFEMAMGYPLQESVVRQITECFE-ALKCLLESILSKEACKAGLPILEQLLGHRFFLQYAS 357

Qy        402 FTS-----   KKPQFKIPTKLKKALPIAKKCIKKKLIKKQKQIHQHRKLIKAQSHHGSEF 454
Db        358 IKSAGAAANAKKPYIKLSLNAKIIIKQAAIKIINPIPIIIIIVENIKRIVPVQELMSSEF 417

Qy        455 EKKEKKILAKKKSKKSALLNS    EEHSARYSNSNNSGSGASSPLT------------S 498
Db        418 EKKESKLKAKLLHKQSKLPQSSIQINNGKISLVAAIAAAASSSTTVVGELCGIPGFNKS 477

Qy        499 PSSPTPPSI-SGISALPPPPPP---------PPPPAAPLPPASTEVPAQLSSQAVNG-  545
Db        478 DSIPKKPITLAGIKSPPLIPGPHLGSIYQQELPSIIGAPVERQSS-TPNMLSEDAEGGDG 536

Qy        546 --MSPGALLSSIQNPQKCILKKAKICD 570
Db        537 DEPTRSALLESICKPNRCSLKKVRGND 563


RESULT 7
O61564
ID   O61564      PRELIMINARY;      PRT;   515 AA.
AC   O61564;
DT   01-AUG-1998 (TrEMBLrel. 07, Created)
DT   01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   SLOB (FRAGMENT).
GN   SLOB OR CG6772.
OS   Drosophila melanogaster (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC   Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7227;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CANTON S;
RA   Schopperle W.M., Holmqvist M.H., Zhou Y., Wang J., Wang Z.,
RA   Griffith L.C., Keselman I., Dagan D., Levitan I.B.;
RL   Neuron 0:0-0(1998).
DR   EMBL; AF051162; AAC06289.1; -.
DR   FlyBase; FBgn0024290; Slob.
FT   NON_TER     515    515
SQ   SEQUENCE   515 AA;  57825 MW;  2185584D9D874FE5 CRC64;

  Query Match             13.1%;  Score 392.5;  DB 5;  Length 515;
  Best Local Similarity   30.3%;  Pred. No. 6.8e-20;
  Matches  122;  Conservative   58;  Mismatches  125;  Indels   97;  Gaps   13;

Qy        145 EWLVVEFLFIIGWRIFKKYIIMKIENQFEERL---  -    VLSWAIIDPPKYLSIKDFQ 196
Db        171 KYLVAHGQLGSHKGKNWLIVIAAVKIIKKQIIIIIIIIVAIIIIINECAK    E 229

Qy        197 IIIIIIIIIIIIYKV       IIIIIIIIIIIIIIIIIIIIIIIIIIIII 251
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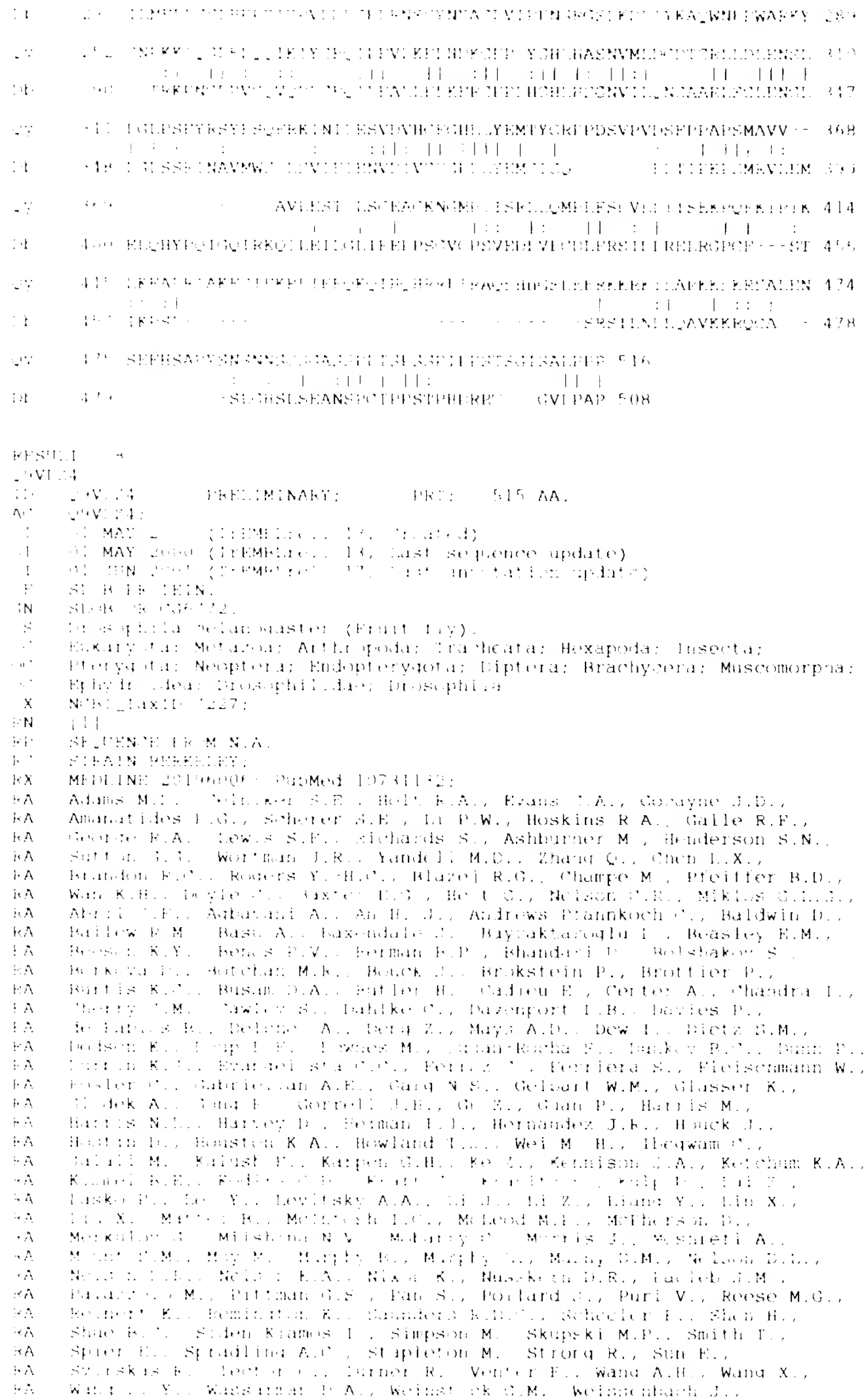
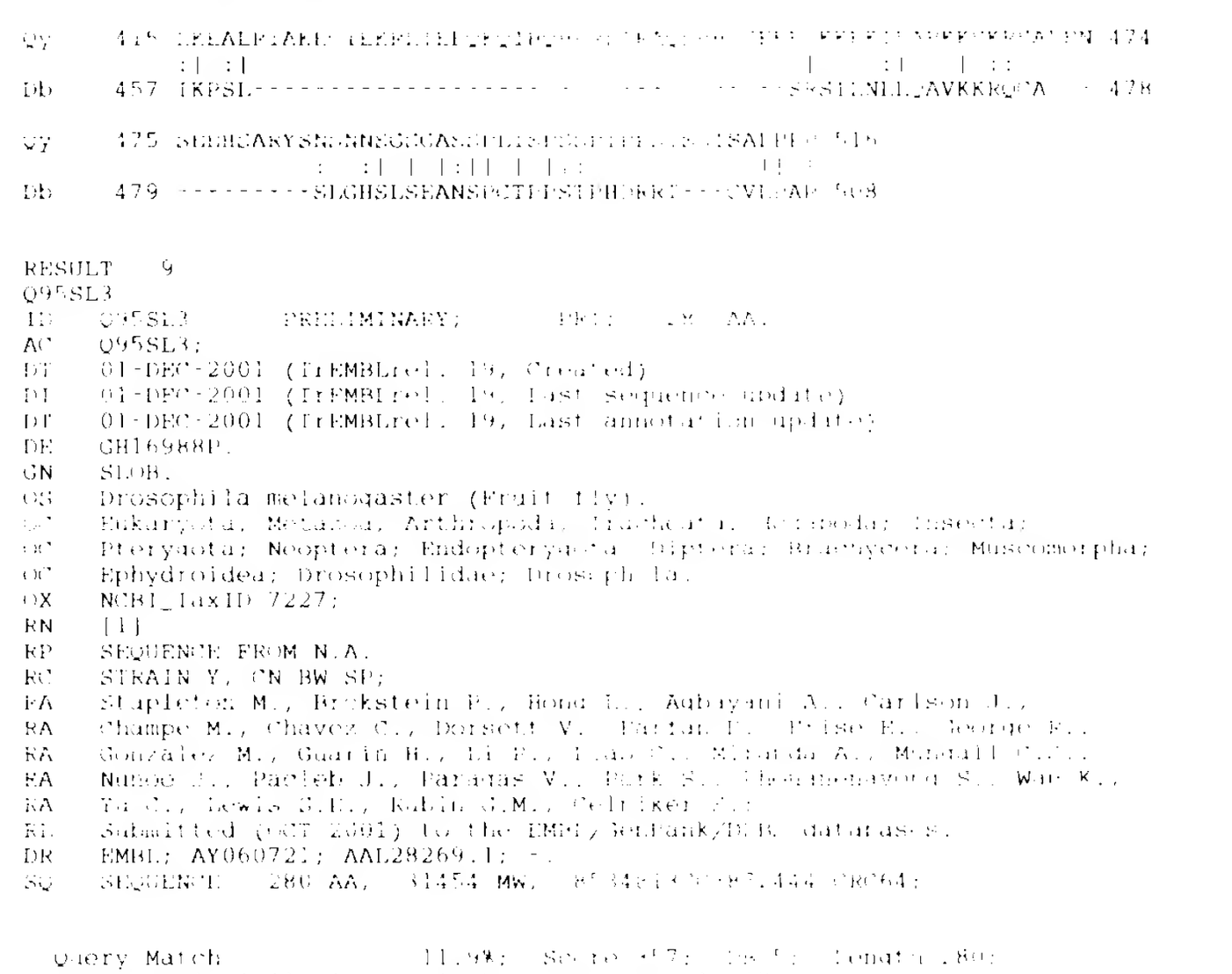


RESULT 8
Q9VL34
ID Q9VL34 PRELIMINARY; PRT: 515 AA.
AC Q9VL34;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 13, Last annotation update)
DE SLOB B CG6722.
GN SLOB OR CG6722.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN BERKELEY;
RX MEDLINE=20196905; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C.,
RA Dunn P., Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zhou X.H., Zhu F.N., Zhang W., Zhao Y., Zhi S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
DR EMBL; AE003618; AAF52534.1; -.
DR FlyBase; FBgn0024290; Slob.
SQ SEQUENCE 515 AA, 57924 MW, [illegible] CRC64;

Query Match 13.1%; Score 492.5; DB 5; Length 515;
Best Local Similarity 30.4%; Pred. No. 5.8e-27;
Matches 122; Conservative 58; Mismatches 125; Indels 37; Gaps 13;



RESULT 9
Q95SL3
ID Q95SL3 PRELIMINARY; PRT: [illegible] AA.
AC Q95SL3;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE GH16988P.
GN SLOB.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN Y, CN BW SP;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
RA Nunoo J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K.,
RA Yu C., Lewis S.E., Rubin G.M., Celniker S.;
RL Submitted (OCT 2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AY060721; AAL28269.1; -.
SQ SEQUENCE 280 AA, 31454 MW, [illegible] CRC64;

Query Match 11.9%; Score 447; DB 5; Length 280;
Best Local Similarity 31.8%; Pred. No. 1e-23;

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Qy      1 MPKTSSCSLLHPYIYSRVI     EATANELSALELIKMENCEVSDDRDKLTKEARELNDLIEKWN 60
            |:|  | |:|:|  |:|:      :: : | | :|  |: :|:|:|||||||  :|: :||
Db      1 MEELLSGGHGTVYKVLHRPTGVIMAVKQIPSVCDEISSERQKLLMDLDISMRTVDCPFTVTFYGALFREGDVWICMELMDTSLDKFYKQVIDKGQTIPEDILGKIAVSIVKALEHLHSKLSVIHRDVKPSNVLINALGQVKMCDFGISGYLVDSVAKTMDAGCKPYMAPERINPELNQKGYNVKSDIWSLGITMIELATGRFPYDSWKTPFQQLKQVVEEPSPQLPADKFSAEFVDFTSQCLKKNSKERPTYPELMQHPFFTLHESKGTDVASFVKLILGDI 240

Qy     61 LPPKELEIGNMEPEFIAEGQKGIQNYLNVIIENHEILCNGELVKEEFLA---------EQ 111
          :|  |:: |   | :|| :|: ||  ::  :     | |   |: ||              |
Db    241 LQQRTIEYERSFEEPFSGVCPSVEDLVLCTDLERSIDEREILRGPCP--STIKPSL 296

Qy    112 LRPNNYSANYTEIALQQVSMFFRSEP--KWEVVEPLKDIG---------WRIRKKYFLMK 167
          :  | :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db    297 LKPNNYCANYTEIALQQVSMFFRSEPGSKWEVVEPLKDIGSKLLQEGGFGSVYKAVHKGYWVMEVAVKMLNVTAPTPQQLQAFKNEVGVLRKTRHVNILLFMGYSTKPQLAIVTQWCEGSSLYHHLHIIETKFEMIKLIDIARQTAQGMDYLHAKSIIHRDLKSNNIFLHEDLTVKIGDFGLATVKSRWSGSQQVEQPTGSVLWMAPEVIRMQDNNPFSFQSDVYSYGIVLYELMTGELPYSHINNRDQIIFMVGRGYLSPDLSKVRSNCPKAMKRLMAECLKKKRDERPLFPQILASIELLARSLPKIHRSASEPSLNRAGFQTEDFSLYACASPKTPIQAGGYGAFPVH 480

Qy    168 IKNQPKEPLVLSWADLGPDKYLSDKDFQVCIKLLPSCLHPYIYRVTFATANESSALLIRM 227
          :    :::::||  :    :    :::::      || :  |:::  : ::         :
Db    481 VLNKPLQLTAEEKSWNLAMTELKTLAQRVQRLGEGHFGSVDLCAFNNEDQNFFVKTVTKVESGDEGYTEFLREASVMTQLRHPNLVQLLGVCTREPPFYIITEFMTYGNLLDYLRECNRQEVSAVVLLYMATQISSAMEYLEKKNFIHRDLAARNCLVGENHLVKVADFGLSRLMTGDTYTAHAGAKFPIKWTAPESLAYNKFSIKSDVWAFGVLLWEIATYGMSPYPGIDLSQVYELLEKDYRMERPEGCPEKVYELMRACWQWNPSDRPSFAEIHQAFETMFQESSISDEVEKELGKQGVRGAVSTLLQAPELPTKTRTSRRAAEHRDTTDVPEMPHSKGQGESDPLDHEPAVSPLLPRKERGPPEGGLNEDERLLPKDKKTNLFSALIKKKKKTAPTPPKRSSFFEMDGYQFDTLQDKEKMKVSLRELQEAASMPKDWRGSWRQCFIDQEEDPSRRDFLSEWDISMTCKIPDEMLPYDAQIDTSDEYEDRILQERTLKVNEWITKGTMLLNRTFRNDPRALVKQMQAKMLDFHMIVENNIQFVPAERDFLHESPMIWNKKKHLVAFVNVSLSEKAQQVYHELFQSCRTDQSNIVVVLHRMEEVMYKSTAYQVGPFTGSGLELPSFQSAVCMRKDEARLKVFTDEIGMSFAFKNLGTDIMTTRRPRDGMLSPVWPESSEVPLTLSFSVFGKGIELTATESTTQLKEVMKEVDIRGLGQDCLYVEVDLAGEDVAFFKGIGPVVGLAKATKKRFQKIPVISIDSVNDKTLYLRDWQETIQVYLDRANVSTVQKHAFQKAVNSLEEPVALLKTVDRWWDSP 720

Qy    228 PNEPCTLKPQDKYKAEVAEDRINDKLRAYLCDPDETLEVDELIAQYYHTLDEEMEGKIQNL 287
          :  |  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db    721 PNEPCTLKPQDKYKAEVAEDRINDKLRAYLCDPDETLEVDELIAQYYHTLDEEMEGKIQNL 780

Qy    288 VGLEMPLDWFVDKPNPECLQEALFTFNHICKPLDNSFTAVPEILQLMLNIITTELPKPAVY 347
          :  |  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db    781 VGLEMPLDWFVDKPNPECLQEALFTFNHICKPLDNSFTAVPEILQLMLNIITTELPKPAVY 840

Qy    348 GSDIDVQLQRDPEVPLSTYNTGEFGCMEMPSKSPKPKPLPPPLPQKDEEKAKNQQVNGHTG 407
          :  |  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db    841 GSDIDVQLQRDPEVPLSTYNTGEFGCMEMPSKSPKPKPLPPPLPQKDEEKAKNQQVNGHTG 900

Qy    408 NEPCASRLPEEIQNHPFEEFERNPFLNEDVNQSKPLPPEDTFIDIDLKSDNPDTPSPQPQS 467
          :  |  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db    901 NEPCASRLPEEIQNHPFEEFERNPFLNEDVNQSKPLPPEDTFIDIDLKSDNPDTPSPQPQS 960

Qy    468 LSAWQFVQEEIP 479
          :  |  :  :  :
Db    961 LSAWQFVQEEIP 972


RESULT  11
Q9ERE3
ID   Q9ERE3       PRELIMINARY;       PRT:   496 AA.
AC   Q9ERE3;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   SERINE/THREONINE-PROTEIN KINASE CISK.
GN   CISK.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE 20504817; PubMed 11050396;
RA   Liu D., Yang X., Songyang Z.;
RT   "Identification of CISK, a new member of the SGK kinase family that
RT   promotes IL-3 dependent survival.";
RL   Curr. Biol. 10:1233-1236(2000).
DR   EMBL; AF312007; AAG34115.1;   .
DR   HSSP; P05132; 1ATP.
DR   InterPro; IPR000719; Euk_pkinase.
DR   InterPro; IPR000961; Pkinase_C.
DR   InterPro; IPR001683; PX.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   Pfam; PF00069; pkinase; 1.
DR   Pfam; PF00433; pkinase_C; 1.
DR   SMART; SM00312; PX; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   SMART; SM00133; S_TK_X; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW   ATP-binding; Kinase; Transferase.
SQ   SEQUENCE   496 AA;  57145 MW;  4871A2804A5948BAD CRC64;


  Query Match              6.8%;  Score 234.5;  DB 11;  Length 496;
  Best Local Similarity   21.0%;  Prod. No. 1.5e-06;
  Matches   96;  Conservative   83;  Mismatches  179;  Indels   99;  Gaps   19;

Qy      17 TVPELTAATEASQSLQSHTEYTIRVQRGTSVENGWQIVRRYSDPDLLNNSL--QIAGLSLP 74
           :|  : :: |  :  :  | | : |  |     : : : :| :|| | |||  |   :::
Db      15 SVSIPGSYGNRREEEEEIVYRVLVVG--EGAWTVRSRYALEDLGLYNPLKEQTPAMALK 71

Qy      75 LPPKELEIGNMEPEFIAEGQKGIQNYLNVIIENHEILCNGELVKEEFLA----------EQ 120
           :| |:: |   | :|| :|: ||  ::  :     | |   |: ||              |
Db      72 IPAKRIEGNFEIDPIKQRRAGLNEPLQNLVEYTELYNHIDVRAATQMESPKHQSSPCED 131

Qy     121 PNNYSANYTEIALQQVSMFFRSEP--KWEVVEPLKDIG----------WRIRKKYFLMK 167
           :  | :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db     132 LDEKSLGRLHSLSNINDPSGNPHAKPFDPGSKVVEGSSPGFVLLAEPFLPCEEYAVK 191

Qy     168 IKNQPKEPLVLSWADLGPDKYLSDKDFQVCIKLLPSCLHPYIYRVTFATANESSALLIRM 227
           :    :::::||  :    :    :::::      || :  |:::  : ::         :
Db     192 VLNKPLQLTAEEKSWNLAMTELKTLAQRVQRLGEGHFGSVDLCAFNNEDQNFFVKTVTKVESGDEGYTEFLREASVMTQLRHPNLVQLLGVCTREPPFYIITEFMTYGNLLDYLRECNRQEVSAVVLLYMATQISSAMEYLEKKNFIHRDLAARNCLVGENHLVKVADFGLSRLMTGDTYTAHAGAKFPIKWTAPESLAYNKFSIKSDVWAFGVLLWEIATYGMSPYPGIDLSQVYELLEKDYRMERPEGCPEKVYELMRACWQWNPSDRPSFAEIHQAFETMFQESSISDEVEKELGKQGVRGAVSTLLQAPELPTKTRTSRRAAEHRDTTDVPEMPHSKGQGESDPLDHEPAVSPLLPRKERGPPEGGLNEDERLLPKDKKTNLFSALIKKKKKTAPTPPKRSSFFEMDGYQFDTLQDKEKMKVSLRELQEAASMPKDWRGSWRQCFIDQEEDPSRRDFLSEWDISMTCKIPDEMLPYDAQIDTSDEYEDRILQERTLKVNEWITKGTMLLNRTFRNDPRALVKQMQAKMLDFHMIVENNIQFVPAERDFLHESPMIWNKKKHLVAFVNVSLSEKAQQVYHELFQSCRTDQSNIVVVLHRMEEVMYKSTAYQVGPFTGSGLELPSFQSAVCMRKDEARLKVFTDEIGMSFAFKNLGTDIMTTRRPRDGMLSPVWPESSEVPLTLSFSVFGKGIELTATESTTQLKEVMKEVDIRGLGQDCLYVEVDLAGEDVAFFKGIGPVVGLAKATKKRFQKIPVISIDSVNDKTLYLRDWQETIQVYLDRANVSTVQKHAFQKAVNSLEEPVALLKTVDRWWDSP 720

Qy     228 PNEPCTLKPQDKYKAEVAEDRINDKLRAYLCDPDETLEVDELIAQYYHTLDEEMEGKIQNL 287
           :  |  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db     721 PNEPCTLKPQDKYKAEVAEDRINDKLRAYLCDPDETLEVDELIAQYYHTLDEEMEGKIQNL 780
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Db    242 EVNGGEL----            -FFHLQRERSFPEPKARFYAAFIASALGYLESIKIVYR 285

Qy    286 HLHASNVMLD[illegible]       D[illegible]CR     [illegible]LD[illegible]LGNSLLGLESFYKSY[illegible]S[illegible]FKKINTLESVD 334

Db    289 [illegible]KFEN[illegible]L[illegible]SMGHVVL[illegible]FGL[illegible]KEGIAISD TFTFCGIPEYLAP--EVIRKQPYDNTVD 343

Qy    335 VHCEGHLLYEMLY[illegible]FPP ---    - DSV --FVDSFLPAPSMAVVAVLESTLSCEACK 381

Db    344 WW[illegible]GAVLYEM[illegible]YG[illegible]FFY[illegible]RDVAEMYDNILHKEL NL[illegible]PGVSL[illegible]AWS[illegible]LEELLE    K 398

Qy    382 N[illegible]ME[illegible]    FI[illegible]QMEL[illegible]SDVLL[illegible]TSEKPQFKIP 412

Db    399 NE[illegible]NML[illegible]AKEP[illegible]NEPPPR[illegible] LEW[illegible]DLVQKKIP 433
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RESULT 12
[illegible]

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ID   [illegible]     PRELIMINARY;     PRT;  1851 AA.
AC   [illegible];
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   [illegible]-JAN-1998 (TrEMBLrel. [illegible], Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. [illegible], Last annotation update)
DE   [illegible] PROTEIN.
GN   [illegible].
OS   Caenorhabditis elegans.
OC   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC   Rhabditidae; Peloderinae; Caenorhabditis.
OX   NCBI_TaxID=[illegible];
RN   [1]
RP   SEQUENCE FROM N.A.
RA   [illegible];
RL   Submitted ([illegible]) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=[illegible]; PubMed=9851916;
RA   none;
RT   "Genome sequence of the nematode C.elegans: A platform for
RT   investigating biology.";
RL   Science 282:2012-2018(1998).
CC   -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR   EMBL; [illegible]; CAA[illegible]2591.1; -.
DR   InterPro; IPR000719; Euk_pkinase.
DR   InterPro; IPR[illegible]; Ser_thr_pkinase.
DR   Pfam; PF00069; pkinase; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW   ATP-binding; Serine/threonine protein kinase; Transferase.
SQ   SEQUENCE   1851 AA;  [illegible] MW;  [illegible] CRC64;

  Query Match             6.1%;  Score 182;  DB 5;  Length 1851;
  Best Local Similarity   22.2%;  Pred. No. 0.00032;
  Matches  [illegible];  Conservative  [illegible];  Mismatches  160;  Indels  146;  Gaps   22;

Qy    17[illegible] [illegible]VLSWA[illegible]KY   [illegible]SDK[illegible]LIKLL[illegible]CLHDY[illegible]YRV[illegible]FATANESSAI---------LI 225

Db    3[illegible] VAVAW[illegible]KLNK[illegible]PPAPMLK[illegible]LQHPNIVR--FYDYWESAL[illegible]CKRKYIVLV 425

Qy    22[illegible] [illegible]IYEAF[illegible]KKY   [illegible]KIYC[illegible]LLEVLE[illegible]LHDKG 283

Db    426 [illegible]K--         - MYLKFFKRINIKVV ------LKSWCRQILKGLSFLHTRN 468

Qy    284 FFY[illegible]H   [illegible]HASNVM[illegible]D[illegible] ---  -CRL[illegible]EN----SL[illegible]GLPSF-----YRSYFSQF 324

Db    46[illegible] [illegible]VIHRD[illegible]NIF[illegible]GSVK[illegible]LAILKNKSPAKSVIGTPEFMAPEMYEEMYD-- 526

Qy    325 KKINT[illegible]ESVDVHC[illegible]GHLLY[illegible]MIYGRPPDS  -  ----------VPVDSFP--PAPSMAV 367

Db    527       ESV[illegible]VYAF[illegible]MC[illegible]LEMV[illegible]MN[illegible]KVI[illegible]VK[illegible]SKIFAQYIEI 580

Qy    368 VAVLESTLS[illegible]EA[illegible]KN[illegible]MPI SRLLQMP[illegible]   ------------- -VLL 401

Db    581 REIIDRCIRVR--REERSTVKQ[illegible]V[illegible]NVE[illegible] 6[illegible]

Qy    402 TTSEKPQFKIPIKLKEALRIAKE[illegible]------ IEK[illegible]       434

Db    639 VYE[illegible]KEF[illegible]Y[illegible]EN[illegible]TAP[illegible]VV[illegible]M[illegible]KLIKDKVDA 698

Qy    435 -K[illegible]IHQ[illegible]RAQSHRCSE[illegible]SAI[illegible]NS[illegible]SAKYSNSNNSGSGAS 493

Db    699 FRRDRDHRLL --EIKRAKFEEKRI[illegible]EAF K[illegible]EAIAK[illegible]EKKEKAAA 755

Qy    494 SPLTSPSSPTPPSTSGISAIPPPPPI[illegible]A- AI[illegible]PASIEVPAQLSSQA 542

Db    756 AAAANP-NPTP------- IPPTPAII[illegible]SSAQQQI[illegible]PIS[illegible]QISAE[illegible]SA 798
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RESULT 13
Q96PY5

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ID   Q96PY5     PRELIMINARY;     PRT;  1112 AA.
AC   Q96PY5;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   KIAA1902 PROTEIN (FRAGMENT).
GN   KIAA1902.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BRAIN;
RX   MEDLINE=21456161; PubMed=11572484;
RA   Nagase T., Kikuno R., Ohara O.;
RT   "Prediction of the coding sequences of unidentified human genes. XXI.
RT   The complete sequences of 60 new cDNA clones from brain which code for
RT   large proteins.";
RL   DNA Res. 8:179-187(2001).
DR   EMBL; AB067489; BAB67795.1; -.
FT   NON_TER      1      1
SQ   SEQUENCE   1112 AA;  126313 MW;  E99D9418934FF[illegible]2B CRC64;

  Query Match             5.9%;  Score 176;  DB 4;  Length 1112;
  Best Local Similarity   19.6%;  Pred. No. 0.00045;
  Matches  120;  Conservative   74;  Mismatches  22[illegible];  Indels  188;  Gaps   21;

Qy     39 EVQECISVENSWCIVERYSDPDLLNNFL[illegible]IACL[illegible]     KKLICNMD-  -    R 86

Db     [illegible] EILFQY[illegible]NEKEWLL[illegible]LEFQVEN         [illegible]VIRKKEK 116

Qy     87 EPIAERQKGLQNYLNVITTNHILSN[illegible]VKK[illegible]NNYGAN  YIE[illegible]AI[illegible]VGMFFRSEF 144

Db    117 KEVQESTQVLKELEISLRTNHI     [illegible]WVKE[illegible]LNEPNK[illegible]AVTFDEES 172

Qy    145 EWEVVE[illegible]KEN[illegible]FRLVI[illegible]LLIKLLLS[illegible] 204

Db    173 VESTVESSVD---------------KSKI -----WSK[illegible]HRGSN -    - LPSP 203

Qy    205 LHPYIYRVTFATANESSALLIEMENEKC[illegible]LKE[illegible]IYEAKEKD[illegible]LKKY[illegible]NIKKIQ[illegible]LEIQQ 264

Db    204 VGNSVSR-- --SGRHSALRYNTLPSKE[illegible]LKNSELV[illegible]KKDDVEVC[illegible]MC    -        246

Qy    265 IKIYGRQILEVLKFLHDKGFFYGHLHASN   VML[illegible]LENSL[illegible]GLPSFYR  - 318

Db    247 ---- - LRAIMNYQYCFNMVMSHPHAVNEIAL[illegible]NNKNPEIEA[illegible]VIEL[illegible]AAV[illegible]LVK[illegible] 299

Qy    319 ----SYFSQFRKI -------- ---- - --N[illegible]LESV              DVHCEGHL 341

Db    300 EIILSAFDNEKEVCGEKQRFEKLMEHFKN[illegible]NNI[illegible]FMVA[illegible]M[illegible]INIVVH[illegible]MNFRVHL 359

Qy    342 LYEMIYGRPPDSVPVDSF        [illegible]PA[illegible]SMAVVAVL[illegible]KN[illegible]ELL[illegible]  392

Db    360 QYEFT      KIGLDEYLDKLKHI[illegible]NV[illegible]VGAL[illegible]KNAALEK 413
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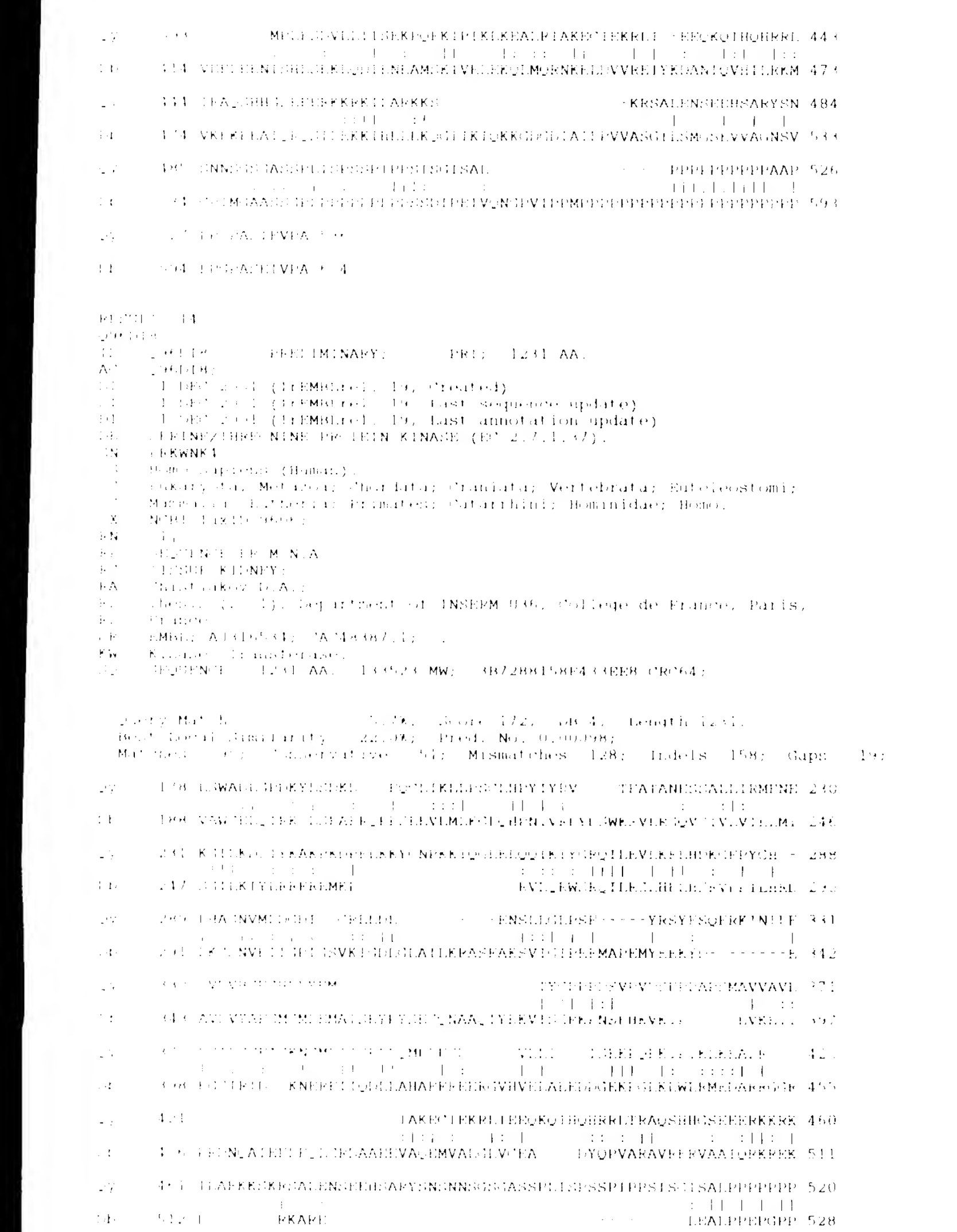

RESULT 14
Q96J92
ID Q96J92 PRELIMINARY; PRT; 1231 AA.
AC Q96J92;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE HYPOTHETICAL 134.7 KDA PROTEIN.
GN PRKWNK4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=KIDNEY;
RX MEDLINE=21390047; PubMed=11498583;
RA Wilson F.H., Disse-Nicodeme S., Choate K.A., Ishikawa K.,
RA Nelson-Williams C., Desitter I., Gunel M., Milford D.V., Lipkin G.W.,
RA Achard J.M., Feely M.P., Dussol B., Berland Y., Unwin R.J., Mayan H.,
RA Simon D.B., Farfel Z., Jeunemaitre X., Lifton R.P.;
RT "Human hypertension caused by mutations in WNK kinases.";
RL Science 293:1107-1112(2001).
DR EMBL; AF390018; AAK91995.1; -.
KW Hypothetical protein.
SQ SEQUENCE 1231 AA; 134723 MW; 8B72B81580F433EE8 CRC64;

Query Match 5.7%; Score 172; DB 4; Length 1231;
Best Local Similarity 22.0%; Pred. No. 0.00098;
Matches 95; Conservative 51; Mismatches 128; Indels 158; Gaps 19;

RESULT 15
Q96J92
ID Q96J92 PRELIMINARY; PRT; 1243 AA.
AC Q96J92;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE HYPOTHETICAL 134.7 KDA PROTEIN.
GN PRKWNK4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=KIDNEY;
RX MEDLINE=21390047; PubMed=11498583;
RA Wilson F.H., Disse-Nicodeme S., Choate K.A., Ishikawa K.,
RA Nelson-Williams C., Desitter I., Gunel M., Milford D.V., Lipkin G.W.,
RA Achard J.M., Feely M.P., Dussol B., Berland Y., Unwin R.J., Mayan H.,
RA Simon D.B., Farfel Z., Jeunemaitre X., Lifton R.P.;
RT "Human hypertension caused by mutations in WNK kinases.";
RL Science 293:1107-1112(2001).
DR EMBL; AF390018; AAK91995.1; -.
KW Hypothetical protein.
SQ SEQUENCE 1243 AA; 134739 MW; BAC49F0898BA4391 CRC64;

Query Match 5.7%; Score 172; DB 4; Length 1243;
Best Local Similarity 22.0%; Pred. No. 0.00099;
Matches 95; Conservative 51; Mismatches 128; Indels 158; Gaps 19;

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